GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 13, 2003, 11:46:42 ; Search time 18.576 Seconds
(without alignments)
2384.805 Million cell updates/sec

Title: US-09-521-335-2
Perfect score: 1169
Sequence: 1 MLACLCTVLWHLPAVPALNR.....KKKMQPPAAAVTLHLGAHGF 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1169	100.0	225	4	Q9UBD9	Q9ubd9 homo sapien
2	1136	97.2	225	11	Q9QZM3	Q9qzm3 mus musculu
3	150.5	12.9	215	13	Q9PUJ2	Q9puj2 plethodon j
4	150.5	12.9	215	13	Q9PUJ1	Q9puj1 plethodon j
5	150.5	12.9	215	13	Q9PUJ0	Q9puj0 plethodon j
6	148.5	12.7	215	13	Q9PUI9	Q9pui9 plethodon j
7	97.5	8.3	530	3	Q8X0E9	Q8x0e9 neurospora
8	94.5	8.1	318	4	Q96LS2	Q96ls2 homo sapien
9	92	7.9	332	10	Q9MAU1	Q9mau1 arabidopsis
10	92	7.9	423	11	Q9JHE4	Q9jhe4 mus musculu
11	92	7.9	455	11	Q9CWV7	Q9cwv7 mus musculu
12	90	7.7	423	11	Q9D8V6	Q9d8v6 mus musculu
13	89	7.6	733	16	Q9I664	Q9i664 pseudomonas
14	88	7.5	771	2	Q9S3Q9	Q9s3q9 porphyromon
15	87	7.4	955	11	O88287	O88287 mus musculu
16	87	7.4	1561	11	O88286	O88286 mus musculu
17	86.5	7.4	640	16	O54153	O54153 streptomyce
18	85.5	7.3	1154	11	Q9Z1R2	Q9z1r2 mus musculu
19	85	7.3	727	11	O88841	O88841 mus musculu
20	84.5	7.2	294	11	Q9CPZ1	Q9cpz1 mus musculu
21	84.5	7.2	389	17	Q9YA71	Q9ya71 aeropyrum p
22	84	7.2	294	4	Q9NXX5	Q9nxx5 homo sapien
23	84	7.2	876	4	Q9P210	Q9p210 homo sapien
24	83.5	7.1	310	4	O95159	O95159 homo sapien
25	83.5	7.1	5990	2	Q9RLP6	Q9rlp6 mycobacteri
26	83	7.1	222	2	Q9L584	Q9l584 streptococc
27	82.5	7.1	310	4	Q9UID0	Q9uid0 homo sapien
28	82.5	7.1	542	16	Q9HTB5	Q9htb5 pseudomonas
29	82	7.0	283	2	Q9ZB87	Q9zb87 pseudomonas
30	82	7.0	611	16	Q98LP5	Q98lp5 rhizobium l
31	82	7.0	721	4	Q96PC8	Q96pc8 homo sapien
32	82	7.0	756	4	Q96PC7	Q96pc7 homo sapien
33	82	7.0	1179	10	O65507	O65507 arabidopsis
34	82	7.0	2376	10	Q9FIN7	Q9fin7 arabidopsis
35	81.5	7.0	396	2	Q9AF00	Q9af00 frankia sp.
36	81.5	7.0	476	11	Q8R363	Q8r363 mus musculu
37	81	6.9	328	15	Q9EI25	Q9ei25 human immun
38	81	6.9	328	15	Q9EI22	Q9ei22 human immun
39	81	6.9	924	2	Q9X582	Q9x582 rhodothermu
40	80.5	6.9	200	16	Q8YBB1	Q8ybb1 brucella me
41	80.5	6.9	305	4	Q9H7R6	Q9h7r6 homo sapien
42	80.5	6.9	466	4	Q96CD4	Q96cd4 homo sapien
43	80.5	6.9	512	13	Q9PSM0	Q9psm0 xenopus lae
44	79.5	6.8	433	10	Q9FI78	Q9fi78 arabidopsis
45	79.5	6.8	924	2	Q9ZIG3	Q9zig3 rhodothermu

ALIGNMENTS

RESULT 1
Q9UBD9
ID Q9UBD9 PRELIMINARY; PRT; 225 AA.
AC Q9UBD9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Neurotrophin-1/B-cell stimulating factor-3 (Cardiotrophin-like
DE cytokine) (Similar to cardiotrophin-like cytokine,
DE neurotrophin-1/B-cell stimulating factor-3).
GN CLC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99432254; PubMed=10500198;
RA Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,
RA Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Manu F.,
RA Simonet W.S., Boone T., Chang M.-S.;
RT "Novel neurotrophin-1/B cell-stimulating factor-3: A cytokine of the
RT IL-6 family.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99382254; PubMed=10448081;
RA Shi Y., Wang W., Yourey P.A., Gohari S., Zukauskas D., Zhang J.,
RA Ruben S., Alderson R.F.;
RT "Computational EST database analysis identifies a novel member of the
RT neuropoietic cytokine family.";
RL Biochem. Biophys. Res. Commun. 262:132-138(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Hu X., Xu Y., Zhang B., Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;

```
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF176912; AAF00992.1; -.
DR   EMBL; AF172854; AAD54284.1; -.
DR   EMBL; AF176911; AAF00991.1; -.
DR   EMBL; AY049779; AAL15436.1; -.
DR   EMBL; BC012939; AAH12939.1; -.
SQ   SEQUENCE   225 AA;  25176 MW;  E2DD4B6280833B55 CRC64;

  Query Match             100.0%;  Score 1169;  DB 4;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-101;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
           |||||||||||||||||||||||||||||||||||
Db     191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225


RESULT 2
Q9QZM3
ID   Q9QZM3      PRELIMINARY;      PRT;   225 AA.
AC   Q9QZM3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Neurotrophin-1/B-cell stimulating factor-3.
GN   BSF3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99432254; PubMed=10500198;
RA   Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,
RA   Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Manu F.,
RA   Simonet W.S., Boone T., Chang M.-S.;
RT   "Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
RT   IL-6 family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).
DR   EMBL; AF176913; AAF00993.1; -.
DR   MGD; MGI:1930088; Bsf3.
SQ   SEQUENCE   225 AA;  25261 MW;  68B1FEAAB7F1A950 CRC64;

  Query Match             97.2%;  Score 1136;  DB 11;  Length 225;
  Best Local Similarity   96.7%;  Pred. No. 3.1e-98;
  Matches  208;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
           ||||||||||||||||||:|||||||||:|||||||||||||||||||||||||||||||
Db      71 EPDFNPPRLGAETLPRATVNLEVWRSLNDRLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
           |||||||||||||||||||| |||||||||||||| | ||||||||||||||||||||||
Db     131 RSLAHFCTSLQGLLGSIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQKMDDFWLLKE 190

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
           |||||||||||||||||||||||||||||||||||
Db     191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLEAHGF 225


RESULT 3
Q9PUJ2
ID   Q9PUJ2      PRELIMINARY;      PRT;   215 AA.
AC   Q9PUJ2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Receptivity factor isoform 1 precursor.
GN   PRF.
OS   Plethodon jordani (Salamander).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
OC   Plethodon.
OX   NCBI_TaxID=8336;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99420364; PubMed=10489368;
RA   Rollmann S.M., Houck L.D., Feldhoff R.C.;
RT   "Proteinaceous pheromone affecting female receptivity in a terrestrial
RT   salamander.";
RL   Science 285:1907-1909(1999).
DR   EMBL; AF181480; AAF01025.1; -.
KW   Signal.
FT   SIGNAL       1     23       POTENTIAL.
SQ   SEQUENCE   215 AA;  24138 MW;  B1906BB666335738 CRC64;

  Query Match             12.9%;  Score 150.5;  DB 13;  Length 215;
  Best Local Similarity   26.2%;  Pred. No. 3.3e-06;
  Matches   42;  Conservative   31;  Mismatches   80;  Indels    7;  Gaps    3;

Qy      46 SLAGTYLNYLGPPFNEPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLC 105
           ||  |||:: | | ::||:  | :    || | :| : :    |: ||  |   || ::
Db      55 SLLPTYLSFQGAPLSDPDYQLPHIKVANLPTAAMDYDTFMKQTDETRLNNNLYFYSAIVE 114

Qy     106 YLR-GLNRQ----AATAELRRSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWT 160
           :|:  :  |      |   |:        :   |:  |: :|  :|  :   ||  :|
Db     115 FLKEAMTEQEDLNPAELSLKAKFEEAMANSNTLISKISDIMTQMGMSVTITLP--KPLVV 172

Qy     161 PGPAHSDFLQKMDDFWLLKELQTWLWRSAKDFNRLKKKMQ 200
           |    : | :|:    : || :  :  : :||  | || |
Db     173 PFEGSAYFRKKLRGGVVCKEYKERVLLTKRDFEFLAKKYQ 212


RESULT 4
Q9PUJ1
ID   Q9PUJ1      PRELIMINARY;      PRT;   215 AA.
AC   Q9PUJ1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Receptivity factor isoform 2 precursor.
GN   PRF.
OS   Plethodon jordani (Salamander).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
OC   Plethodon.
OX   NCBI_TaxID=8336;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99420364; PubMed=10489368;
RA   Rollmann S.M., Houck L.D., Feldhoff R.C.;
RT   "Proteinaceous pheromone affecting female receptivity in a terrestrial
RT   salamander.";
RL   Science 285:1907-1909(1999).
DR   EMBL; AF181481; AAF01026.1; -.
KW   Signal.
FT   SIGNAL       1     23       POTENTIAL.
SQ   SEQUENCE   215 AA;  24080 MW;  B341B8B7B4E28438 CRC64;
```

```
                 || |:  | | |   |  : |: |        | |||      :: |  ::  |:
Db      84 ---SERLRQDAAALSALPALLDAVRRRQAELNPRAPRLLRSLEDAARQVRALGAAVETVL 140

Qy     142 AALGY----PLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKELQTWLWRSAKDFNRL 195
           ||||     |:|:|:  |   :|   |   |  |:    :       |: |:  |  :|
Db     141 AALGAAARGPVPEPV-ATSALFTSNSAAGVFSAKVLGLHVCGLYGEWVSRTEGDLGQL 197


RESULT 2
CTF1_MOUSE
ID   CTF1_MOUSE      STANDARD;      PRT;   203 AA.
AC   Q60753;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Cardiotrophin-1 (CT-1).
GN   CTF1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
     NCBI_TaxID=10090;
     [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95166785; PubMed=7862649;
RA   Pennica D., King K.L., Shaw K.J., Luis E., Rullamas J., Luoh S.-M.,
RA   Darbonne W.C., Knutzon D.S., Yen R., Chien K.R., Baker J.B.,
RA   Wood W.I.;
RT   "Expression cloning of cardiotrophin 1, a cytokine that induces
RT   cardiac myocyte hypertrophy.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:1142-1146(1995).
CC   -!- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO
CC       AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
CC       RECEPTOR)/GP 130 RECEPTOR COMPLEX.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,
CC       LIVER, LUNG AND KIDNEY. LOWER LEVELS IN TESTIS AND BRAIN. NO
CC       EXPRESSION IN SPLEEN.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U18366; AAC52173.1; -.
     MGD; MGI:105115; Ctf1.
     Cytokine.
SQ   SEQUENCE   203 AA;  21509 MW;  8B3D414A0B3B232F CRC64;

  Query Match             10.1%;  Score 118.5;  DB 1;  Length 203;
  Best Local Similarity   28.8%;  Pred. No. 0.00046;
  Matches   51;  Conservative   21;  Mismatches   88;  Indels   17;  Gaps    5;

Qy      30 IQKTYDLTRYLEHQLRSLAGTYLNYLGPPFNEPDFNPPRL---GAETLPRATVDLEVWRS 86
           |::|::| | |       |   |:   | ||  | |:||||   |      :   | |
Db      27 IRQTHNLARLLTKYAEQLLEEYVQQQGEPFGLPGFSPPRLPLAGLSGPAPSHAGLPV--- 83

Qy      87 LNDKLRLTQNYEAYSHLLCYLRGLNRQAA-----TAELRRSLAHFCTSLQGLLGSIAGVM 141
                || |:  | | |   |  : |: |        | |||      :: |  ::  |:
Db      84 ---SERLRQDAAALSVLPALLDAVRRRQAELNPRAPRLLRSLEDAARQVRALGAAVETVL 140

Qy     142 AALGYPL--PQPLPGTEPT-WTPGPAHSDFLQKMDDFWLLKELQTWLWRSAKDFNRL 195
           ||||     | | | |  | :|       |  |:  | :      |: |:  |  :|
Db     141 AALGAAARGPGPEPVTVATLFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQL 197


RESULT 3
CST_MOUSE
ID   CST_MOUSE      STANDARD;      PRT;   423 AA.
AC   Q9JHE4; Q9D8V6;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Galactosylceramide sulfotransferase (EC 2.8.2.11) (GalCer
DE   sulfotransferase) (Cerebroside sulfotransferase) (3'-
DE   phosphoadenylylsulfate:galactosylceramide 3'-sulfotransferase)
DE   (3'-phosphoadenosine-5'phosphosulfate:GalCer sulfotransferase).
GN   CST OR GCST.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC   TISSUE=Kidney;
RX   PubMed=10727929;
RA   Hirahara Y., Tsuda M., Wada Y., Honke K.;
RT   "cDNA cloning, genomic cloning, and tissue-specific regulation of
RT   mouse cerebroside sulfotransferase.";
RL   Eur. J. Biochem. 267:1909-1917(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   FUNCTION.
RX   PubMed=11917099;
RA   Honke K., Hirahara Y., Dupree J., Suzuki K., Popko B., Fukushima K.,
RA   Fukushima J., Nagasawa T., Yoshida N., Wada Y., Taniguchi N.;
RT   "Paranodal junction formation and spermatogenesis require
RT   sulfoglycolipids.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:4227-4232(2002).
CC   -!- FUNCTION: Catalyzes the sulfation of membrane glycolipids. Seems
CC       to prefer beta-glycosides at the nonreducing termini of sugar
CC       chains attached to a lipid moiety. Catalyzes the synthesis of
CC       HSO3-3-galactosylceramide (sulfatide), a major lipid component of
CC       the myelin sheath and of HSO3-3-monogalactosylalkylacylglycerol
CC       (seminolipid), present in spermatocytes. Also acts on
CC       lactosylceramide, galactosyl 1-alkyl-2-sn-glycerol and galactosyl
CC       diacylglycerol (in vitro).
CC   -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a
CC       galactosylceramide = adenosine 3',5'-bisphosphate +
CC       galactosylceramide sulfate.
CC   -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate +
CC       monogalactosylalkylacylglycerol = adenosine 3',5'-bisphosphate +
CC       monogalactosylalkylacylglycerol sulfate.
CC   -!- PATHWAY: Sphingolipid and glycerolipid biosynthesis.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 13, 2003, 11:41:52 ; Search time 6.192 Seconds
(without alignments)
1440.150 Million cell updates/sec

Title: US-09-521-335-2
Perfect score: 1169
Sequence: 1 MLACLCTVLWHLPAVPALNR.....KKKMQPPAAAVTLHLGAHGF 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	124.5	10.7	203	1	CTF1_RAT	Q63086 rattus norv
2	118.5	10.1	203	1	CTF1_MOUSE	Q60753 mus musculu
3	94	8.0	423	1	CST_MOUSE	Q9jhe4 m galactosy
4	91.5	7.8	201	1	CTF1_HUMAN	Q16619 homo sapien
5	91	7.8	195	1	CNTF_CHICK	Q02011 gallus gall
6	91	7.8	1182	1	HAIR_MOUSE	Q61645 mus musculu
7	89.5	7.7	1313	1	MIP1_SCHPO	P87141 schizosacch
8	87.5	7.5	1181	1	HAIR_RAT	P97609 rattus norv
9	86	7.4	1009	1	M2B2_HUMAN	Q9y2e5 homo sapien
10	85.5	7.3	560	1	PHAC_PSEOL	P26496 pseudomonas
11	84	7.2	200	1	CNTF_PIG	O02732 sus scrofa
12	84	7.2	619	1	NXF1_HUMAN	Q9ubu9 homo sapien
13	83	7.1	452	1	TLL_DROME	P18102 drosophila
14	81.5	7.0	1189	1	HAIR_HUMAN	O43593 homo sapien
15	81	6.9	291	1	YM32_MYCTU	Q10515 mycobacteri
16	81	6.9	724	1	P85B_BOVIN	P23726 bos taurus
17	80.5	6.9	294	1	HUPK_RHOCA	P30797 rhodobacter
18	80.5	6.9	870	1	BCA1_HUMAN	P56945 homo sapien
19	80	6.8	200	1	CNTF_RAT	P20294 rattus norv
20	79	6.8	1621	1	ALK_MOUSE	P97793 mus musculu
21	78.5	6.7	390	1	YL28_STRCO	P40181 streptomyce
22	78.5	6.7	1102	1	CARB_STRCO	Q9kxr6 streptomyce
23	78	6.7	3680	1	DMD_CANFA	O97592 canis famil
24	77	6.6	586	1	UL84_HCMVA	P16727 human cytom
25	77	6.6	587	1	UL84_HCMVT	P29839 human cytom
26	76.5	6.5	572	1	SYM_AERPE	Q9ycy3 aeropyrum p
27	76.5	6.5	618	1	NXF1_RAT	O88984 rattus norv
28	76.5	6.5	995	1	M2B2_PIG	Q28949 sus scrofa
29	76	6.5	1001	1	PTPX_MOUSE	P80560 mus musculu
30	76	6.5	1132	1	BAT3_HUMAN	P46379 homo sapien
31	75.5	6.5	422	1	Y140_HUMAN	Q14153 homo sapien
32	75.5	6.5	830	1	VPP3_HUMAN	Q13488 h vacuolar
33	75	6.4	199	1	CNTF_RABIT	P14188 oryctolagus
34	75	6.4	315	1	YNEF_ECOLI	P76147 escherichia
35	75	6.4	343	1	DFRA_SYNY3	P73212 synechocyst
36	75	6.4	450	1	TLL_DROVI	O16845 drosophila
37	75	6.4	917	1	SYI_STAAU	P41972 staphylococ
38	75	6.4	1620	1	ALK_HUMAN	Q9um73 homo sapien
39	75	6.4	2261	1	RRPL_MUMPM	P30929 mumps virus
40	74.5	6.4	346	1	YG2Q_YEAST	P53259 saccharomyc
41	74.5	6.4	409	1	NER1_MOUSE	O35657 mus musculu
42	74	6.3	508	1	EGR1_RAT	P08154 rattus norv
43	74	6.3	859	1	YDBB_SCHPO	Q10362 schizosacch
44	73.5	6.3	628	1	DXS_AQUAE	O67036 aquifex aeo
45	73.5	6.3	1009	1	FAK2_HUMAN	Q14289 h protein t

ALIGNMENTS

RESULT 1
CTF1_RAT
ID CTF1_RAT STANDARD; PRT; 203 AA.
AC Q63086;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Cardiotrophin-1 (CT-1).
GN CTF1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Heart;
RX MEDLINE=96193659; PubMed=8604995;
RA Ishikawa M., Saito Y., Miyamoto Y., Kuwahara K., Ogawa E.,
RA Nakagawa O., Harada M., Masuda I., Nakao K.;
RT "cDNA cloning of rat cardiotrophin-1 (CT-1): augmented expression of
RT CT-1 gene in ventricle of genetically hypertensive rats.";
RL Biochem. Biophys. Res. Commun. 219:377-381(1996).
CC -!- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO
CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
CC RECEPTOR)/GP 130 RECEPTOR COMPLEX.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRICLE AND ATRIUM OF ADULT
CC RATS. ALSO DETECTED IN THE LUNG, KIDNEY, LIVER, SKELETAL MUSCLE,
CC STOMACH AND URINARY BLADDER. NOT DETECTED IN BRAIN, COLON, TESTIS,
CC SPLEEN OR THYMUS. OVEREXPRESSED IN THE VENTRICULES IN THE CASE OF
CC HYPERTENSION AND HYPERTROPHY.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC ----------

CC ----------
DR EMBL; D78591; BAA11427.1; -.
DR InterPro; IPR001581; LIF_OSM.
DR SMART; SM00080; LIF_OSM; 1.
KW Cytokine.
SQ SEQUENCE 203 AA; 21439 MW; DF8B921A2FA1C832 CRC64;

Query Match 10.7%; Score 124.5; DB 1; Length 203;
Best Local Similarity 28.1%; Pred. No. 0.00012;
Matches 50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;

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Qy      30 IQKTYDLTRYLEHQLRSLAGTYLNYLGPPFNEPDFNPPRL---GAETLPRATVDLEVWRS 86
           |::|::| | |       |   |:   | ||  | |:||||   |       :   | |
Db      27 IRQTHNLARLLTKYADQLLEEYVQQQGEPPGLPGFSPPRLPLAGLSGPAPSHAGLPV--- 83

Qy      87 LNDKLRLTQNYEAYSHLLCYLRGLNRQAA-----TAELRRSLAHFCTSLQGLLGSIAGVM 141
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```
C;Keywords: cytokine; glycoprotein
F;164/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             10.1%;  Score 118.5;  DB 2;  Length 203;
  Best Local Similarity   28.8%;  Pred. No. 0.0014;
  Matches   51;  Conservative   21;  Mismatches   88;  Indels   17;  Gaps    5;

Qy      30 IQKTYDLTRYLEHQLRSLAGTYLNYLGPPFNEPDFNPPRL---GAETLPRATVDLEVWRS 86
           |::|::| | |       |   |:   | ||  | |:|||    |       :   | |
Db      27 IRQTHNLARLLTKYAEQLLEEYVQQQGEPFGLPGFSPPRLPLAGLSGPAPSHAGLPV--- 83

Qy      87 LNDKLRLTQNYEAYSHLLCYLRGLNRQAA-----TAELRRSLAHFCTSLQGLLGSIAGVM 141
           || |:  | | |   | : |: |         | |||      :: |  ::  |:
Db      84 ---SERLRQDAAALSVLPALLDAVRRRQAELNPRAPRLLRSLEDAARQVRALGAAVETVL 140

Qy     142 AALGYPL--PQPLPGTEPT-WTPGPAHSDFLQKMDDFWLLKELQTWLWRSAKDFNRL 195
           ||||     | | | | | :|       |  |:  | :      |: |:  |  :|
Db     141 AALGAAARGPGPEPVTVATLFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQL 197


RESULT 3
G86182
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G86182
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332 <STO>
A;Cross-references: GB:AE005172; NID:g7211973; PIDN:AAF40444.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

  Query Match             7.9%;  Score 92;  DB 2;  Length 332;
  Best Local Similarity   26.4%;  Pred. No. 0.76;
  Matches   58;  Conservative   24;  Mismatches   72;  Indels   66;  Gaps   13;

Qy      13 PAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNY----------------- 54
           |:| | | :| | | ||   |||    | : |: ||    ::
Db     113 PSVTAGNLSGYP-PRPSF--TYDPGPYEQRQMESLLQQFIRERNPQIRPLPRLGLGSPVG 169

Qy      55 LGPPFNEPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQA 114
           |||    | |  ||:     | : :|     | | | |       :    | :||  |:
Db     170 LGPIRASPQFLQPRVAPP--PTSILD----TSRNRKAR------SKDGALAVVRG--RKV 215

Qy     115 ATAELRRSL-----------AHFCTSLQGLLGSIAGVMAALGYPLPQPLP---GTEPTWT 160
           |   ||            ||      |:    :|:|     |||:|||    || :
Db     216 RITEGSSSLYSLGRSWLKNGAHV-----GIQPQRSGIMK----PLPKPLPVDLTTETSVP 266

Qy     161 PGPAHSDFLQKMDDFWLLKELQTWLWRSAKDFNRLKKKMQ 200
           |      :  :|   :|:|      | ||   ||: ::
Db     267 DDPDEESADEDKEDEEAVKQL------SEKDL--LKRHIE 298


RESULT 4
G02312
cardiotrophin-1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C;Accession: G02312
R;Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01035
A;Accession: G02312
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-201 <WOO>
A;Cross-references: EMBL:U43030; NID:g1151149; PID:g1151150
C;Genetics:
A;Gene: GDB:CTF1; CT-1
A;Cross-references: GDB:567078
A;Map position: 1p22-1p22

  Query Match             7.8%;  Score 91.5;  DB 2;  Length 201;
  Best Local Similarity   25.9%;  Pred. No. 0.45;
  Matches   45;  Conservative   24;  Mismatches   92;  Indels   13;  Gaps    5;

Qy      30 IQKTYDLTRYLEHQLRSLAGTYLNYLGPPFNEPDFNPPRLGAETLPRATVDLEVWRSLND 89
           |::|: |   |       |   |:   | ||  | |:||||    |  |          :::
Db      27 IRQTHSLAHLLTKYAEQLLQEYVQLQGDPFGLPSFSPPRLPVAGL-SAPAPSHAGLPVHE 85

Qy      90 KLRLTQNYEAYSHLLCYLRGLNRQAA-----TAELRRSLAHFCTSLQGLLGSIAGVMAAL 144
           :|||  :  | : |   |  : |: |         | | |      : |  ::  ::|||
Db      86 RLRL--DAAALAALPPLLDAVCRRQAELNPRAPRLLRRLEDAARQARALGAAVEALLAAL 143

Qy     145 GYPLPQPLPGTEP---TWTPGPAHSDFLQKMDDFWLLKELQTWLWRSAKDFNRL 195
           |       |  ||   | :   |   |  |:    :    : || |:  |  :|
Db     144 G--AANRGPRAEPPAATASAASATGVFPAKVLGLRVCGLYREWLSRTEGDLGQL 195


RESULT 5
JH0680
ciliary neurotrophic factor - chicken
N;Alternate names: growth-promoting activity protein
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C;Accession: JH0680; PQ0057
R;Leung, D.W.; Parent, A.S.; Cachianes, G.; Esch, F.; Coulombe, J.N.; Nikolics, K.; Ecker
Neuron 8, 1045-1053, 1992
A;Title: Cloning, expression during development, and evidence for release of a trophic fa
A;Reference number: JH0680; MUID:92304573; PMID:1610564
A;Accession: JH0680
A;Molecule type: mRNA
A;Residues: 1-195 <LEU>
A;Cross-references: GB:M80827; NID:g211822; PIDN:AAA48784.1; PID:g211823
A;Experimental source: eye
R;Eckenstein, F.P.; Esch, F.; Holbert, T.; Blacher, R.W.; Nishi, R.
Neuron 4, 623-631, 1990
A;Title: Purification and characterization of a trophic factor for embryonic peripheral r
A;Reference number: PQ0057; MUID:90211978; PMID:2322465
A;Accession: PQ0057
A;Molecule type: protein
A;Residues: 155-166,'X',168-175 <ECK>
A;Experimental source: sciatic nerves
C;Comment: This is a neurotrophic protein.
C;Superfamily: ciliary neurotrophic factor
C;Keywords: growth factor

  Query Match             7.8%;  Score 91;  DB 2;  Length 195;
  Best Local Similarity   27.3%;  Pred. No. 0.48;
  Matches   51;  Conservative   21;  Mismatches   83;  Indels   32;  Gaps    9;

Qy      36 LTRYLEHQLRSLAGTYLNYLGPPFNEPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQ 95
           | | :   :  |   |:   |      | :       : :| | |  | |        ||
Db      23 LARKMRSDVTDLLDIYVERQG-----LDASISVAAVDGVPTAAV--ERWAEQTGTQRLLD 75

Qy      96 N---YEAYSHLLCYLRGLNRQA---ATAELRRSLA-------HFCTSLQGLLGSIAGVMA 142
           |   | |:  ||  :    |:      |||  :||         |   |: ||      :
Db      76 NLAAYRAFRTLLAQMLEEQRELLGDTDAELGPALAAMLLQVSAFVYHLEELL-----ELE 130

Qy     143 ALGYPLPQPLPGTEPTWTPGPAH-SDFLQKMDDFWLLKELQTWLWRSAKDFNRLKKKMQP 201
           : | |  :   |:||   | |   | | ||:    :|:||  |  || :|  :| |
Db     131 SRGAPAEE---GSEP---PAPPRLSLFEQKLRGLRVLRELAQWAVRSVRDLRQLSKHGPG 184
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 13, 2003, 11:48:13 ; Search time 9.632 Seconds
(without alignments)
2145.858 Million cell updates/sec

Title: US-09-521-335-2
Perfect score: 1169
Sequence: 1 MLACLCTVLWHLPAVPALNR.....KKKMQPPAAAVTLHLGAHGF 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	124.5	10.7	203	2	JC4645	cardiotrophin-1 -
2	118.5	10.1	203	2	I49153	cardiotrophin-1 -
3	92	7.9	332	2	G86182	hypothetical prote
4	91.5	7.8	201	2	G02312	cardiotrophin-1 -
5	91	7.8	195	2	JH0680	ciliary neurotroph
6	91	7.8	1182	2	I48378	hairless protein -
7	89.5	7.7	1313	2	T38943	probable guanine n
8	89	7.6	733	2	D83588	conserved hypothet
9	87	7.4	955	2	T00247	zinc finger protei
10	87	7.4	1561	2	T00248	zinc finger protei
11	86.5	7.4	640	2	T34916	transferase - Stre
12	85.5	7.3	560	2	C38604	poly(3-hydroxyalka
13	84.5	7.2	389	2	F72511	probable cystathio
14	83	7.1	452	2	A35602	tailless (tll) pro
15	82.5	7.1	542	2	A82965	hypothetical prote
16	82	7.0	1179	2	T04584	TMV resistance pro
17	81.5	7.0	723	2	B38749	3-phosphatidylinos
18	80.5	6.9	200	2	AD3633	hypothetical prote
19	80.5	6.9	512	2	S21171	activin receptor S
20	80	6.8	200	1	UNRTCF	ciliary neurotroph
21	79	6.8	353	2	AB1823	hypothetical prote
22	79	6.8	559	2	G71327	probable apolipopr
23	79	6.8	812	2	T34180	hypothetical prote
24	79	6.8	1220	2	AD0125	exodeoxyribonuclea
25	79	6.8	1621	2	T30200	protein-tyrosine k
26	78.5	6.7	390	2	T35509	hypothetical prote
27	78.5	6.7	426	2	AI0287	conserved hypothet
28	78.5	6.7	460	2	D75493	cell division cycl
29	78	6.7	254	2	T08755	yes-associated pro
30	78	6.7	272	2	T35231	hypothetical prote
31	77.5	6.6	7463	2	T36248	CDA peptide synthe
32	77	6.6	520	2	B75332	extracellular solu
33	77	6.6	586	1	WMBEDE	65K early nonstruc
34	77	6.6	587	1	WMBETE	65K early nonstruc
35	77	6.6	733	2	F82965	hypothetical prote
36	76.5	6.5	310	2	A82734	conserved hypothet
37	76.5	6.5	338	2	T45394	hypothetical prote
38	76.5	6.5	522	2	D87123	conserved hypothet
39	76.5	6.5	572	2	B72714	probable methionyl
40	76.5	6.5	837	2	T12514	hypothetical prote
41	76.5	6.5	1006	2	T42762	probable alpha-man
42	76	6.5	531	2	B83422	probable serine/th
43	76	6.5	1007	2	E72489	hypothetical prote
44	76	6.5	1031	2	F83561	probable DNA polym
45	76	6.5	1132	2	A35098	MHC class III hist

ALIGNMENTS

RESULT 1
JC4645
cardiotrophin-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
C;Accession: JC4645
R;Ishikawa, M.; Saito, Y.; Miyamoto, Y.; Kuwahara, K.; Ogawa, E.; Nakagawa, O.; Harada, M
Biochem. Biophys. Res. Commun. 219, 377-381, 1996
A;Title: cDNA cloning of rat cardiotrophin-1 (CT-1): Augmented expression of CT-1 gene ir
A;Reference number: JC4645; MUID:96193659; PMID:8604995
A;Accession: JC4645
A;Molecule type: mRNA
A;Residues: 1-203 <ISH>
A;Cross-references: DDBJ:D78591; NID:g1256926; PIDN:BAA11427.1; PID:g1256927
C;Genetics:
A;Gene: CT-1
C;Keywords: cardiac muscle; cytokine; heart

Query Match 10.7%; Score 124.5; DB 2; Length 203;
Best Local Similarity 28.1%; Pred. No. 0.00039;
Matches 50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;

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Qy      30 IQKTYDLTRYLEHQLRSLAGTYLNYLGPPFNEPDFNPPRL---GAETLPRATVDLEVWRS 86
           |::|::| | |       |   |:   | ||  | |:||||   |       :   | ||
Db      27 IRQTHNLARLLTKYADQLLEEYVQQQGEPFGLPGFSPPRLPLAGLSGPAPSHAGLPV--- 83

Qy      87 LNDKLRLTQNYEAYSHLLCYLRGLNRQAA-----TAELRRSLAHFCTSLQGLLGSIAGVM 141
              || |:  | | |   |  : |: |         | |||       :: |  ::  |:
Db      84 ---SERLRQDAAALSALPALLDAVRRRQAELNPRAPRLLRSLEDAARQVRALGAAVETVL 140

Qy     142 AALGY----PLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKELQTWLWRSAKDFNRL 195
           ||||     |:|:|:  |   :|   |   |   |:    :       |: |:  |  :|
Db     141 AALGAAARGPVPEPV-ATSALFTSNSAAGVFSAKVLGLHVCGLYGEWVSRTEGDLGQL 197
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RESULT 2
I49153
cardiotrophin-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I49153
R;Pennica, D.; King, K.L.; Shaw, K.J.; Luis, E.; Rullamas, J.; Luoh, S.; Darbonne, W.C.;
Proc. Natl. Acad. Sci. U.S.A. 92, 1142-1146, 1995
A;Title: Expression cloning of cardiotrophin 1, a cytokine that induces cardiac myocyte h
A;Reference number: I49153; MUID:95166785; PMID:7862649
A;Accession: I49153
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-203 <RES>
A;Cross-references: EMBL:U18366; NID:g710331; PIDN:AAC52173.1; PID:g710332
C;Genetics:
A;Gene: ctf1

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RESULT 2
US-09-931-704-5
; Sequence 5, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
;  APPLICANT: Senaldi, Giorgio
;  TITLE OF INVENTION: Methods and Compositions for Treating IgE-Related Disease Using N
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: A-695
;  CURRENT APPLICATION NUMBER: US/09/931,704
;  CURRENT FILING DATE:  2001-08-16
;  PRIOR APPLICATION NUMBER: US 60/226,436
;  PRIOR FILING DATE: 2000-08-18
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Murine
US-09-931-704-5

  Query Match             97.2%;  Score 1136;  DB 10;  Length 225;
  Best Local Similarity   96.7%;  Pred. No. 2e-105;
  Matches  208;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
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Db      11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
           ||||||||||||||||||:|||||||||:||||||||||||||||||||||||||||||||
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Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
           |||||||||||||||||||||| |||||||||||||| | ||||||||||||||||||||
Db     131 RSLAHFCTSLQGLLGSIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQKMDDFWLLKE 190

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
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Db     191 LQTWLWRSAKDFNRLKKKMQPPAASVTLHLEAHGF 225


RESULT 3
US-09-864-761-40014
; Sequence 40014, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40014
;   LENGTH: 164
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC005849.1
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.4
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
;   OTHER INFORMATION: EST_HUMAN HIT: AI752561.1, EVALUE 3.00e-66
;   OTHER INFORMATION: SWISSPROT HIT: Q63086, EVALUE 8.00e-03
US-09-864-761-40014

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  Best Local Similarity   99.4%;  Pred. No. 1.2e-80;
  Matches  163;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     112 RQAATAELRRSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQK 171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 RQAATAELRRSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQK 120

Qy     172 MDDFWLLKELQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
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Db     121 MDDFWLLKELQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 164


RESULT 4
US-09-896-856-3
; Sequence 3, Application US/09896856
; Patent No. US20020137189A1
;   GENERAL INFORMATION:
;        APPLICANT: Baker, Joffre
;                   Chien, Kenneth
;                   King, Kathleen
;                   Pennica, Diane
;                   Wood, William
;        TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 13, 2003, 11:49:27 ; Search time 8.256 Seconds
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1169	100.0	225	10	US-09-931-704-2	Sequence 2, Appli
2	1136	97.2	225	10	US-09-931-704-5	Sequence 5, Appli
3	885	75.7	164	10	US-09-864-761-40014	Sequence 40014, A
4	118.5	10.1	203	10	US-09-896-856-3	Sequence 3, Appli
5	91.5	7.8	201	10	US-09-901-540-3	Sequence 3, Appli
6	91.5	7.8	201	10	US-09-896-856-8	Sequence 8, Appli
7	91.5	7.8	201	10	US-09-901-257-3	Sequence 3, Appli
8	91	7.8	195	10	US-09-770-361-5	Sequence 5, Appli
9	91	7.8	1182	9	US-10-024-368-6	Sequence 6, Appli
10	90	7.7	232	10	US-09-810-052-2	Sequence 2, Appli
11	90	7.7	242	9	US-10-000-776-2	Sequence 2, Appli
12	90	7.7	242	9	US-09-791-497-2	Sequence 2, Appli
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15	90	7.7	243	10	US-09-810-052-5	Sequence 5, Appli
16	87.5	7.5	1207	9	US-10-024-368-5	Sequence 5, Appli
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18	81.5	7.0	218	10	US-09-893-737-28	Sequence 28, Appl
19	81.5	7.0	984	9	US-10-024-368-2	Sequence 2, Appli
20	81.5	7.0	1189	9	US-10-024-368-4	Sequence 4, Appli
21	81	6.9	200	10	US-09-770-361-6	Sequence 6, Appli
22	79	6.8	418	9	US-09-946-807-3	Sequence 3, Appli
23	79	6.8	418	10	US-09-795-668-3	Sequence 3, Appli
24	79	6.8	418	10	US-09-795-686-3	Sequence 3, Appli
25	77.5	6.6	200	10	US-09-770-361-10	Sequence 10, Appl
26	77.5	6.6	379	9	US-09-860-846-16	Sequence 16, Appl
27	77.5	6.6	379	10	US-09-861-289-16	Sequence 16, Appl
28	77.5	6.6	625	10	US-09-771-161A-242	Sequence 242, App
29	77.5	6.6	625	10	US-09-771-161A-243	Sequence 243, App
30	77.5	6.6	3782	9	US-09-860-846-4	Sequence 4, Appli
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32	77	6.6	439	12	US-10-078-929-60	Sequence 60, Appl
33	76	6.5	348	10	US-09-730-617-2	Sequence 2, Appli
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35	76	6.5	451	10	US-09-764-864-1344	Sequence 1344, Ap
36	75.5	6.5	1040	9	US-09-988-626-238	Sequence 238, App
37	75.5	6.5	1040	9	US-09-988-687-238	Sequence 238, App
38	75	6.4	199	10	US-09-770-361-3	Sequence 3, Appli
39	75	6.4	917	10	US-09-815-242-5603	Sequence 5603, Ap
40	75	6.4	920	10	US-09-815-242-12181	Sequence 12181, A
41	75	6.4	920	10	US-09-815-242-12995	Sequence 12995, A
42	75	6.4	920	10	US-09-815-242-13148	Sequence 13148, A
43	75	6.4	1620	10	US-09-827-949-2	Sequence 2, Appli
44	73.5	6.3	1009	8	US-08-987-689A-2	Sequence 2, Appli
45	72.5	6.2	231	9	US-10-000-776-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-931-704-2
; Sequence 2, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating IgE-Related Disease Using NI
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-704-2

Query Match 100.0%; Score 1169; DB 10; Length 225;
Best Local Similarity 100.0%; Pred. No. 1e-108;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
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Db     191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225
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  Matches  208;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
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Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
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Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
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Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
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RESULT 7
[redacted]-016-534-5
; Sequence 5, Application US/09016534
; Patent No. 6143874
;  GENERAL INFORMATION:
;    APPLICANT:  CHANG, MING-SHI
;    APPLICANT:  ELLIOTT, GARY S.
;    APPLICANT:  SARMIENTO, ULLA
;    APPLICANT:  SENALDI, GIORGIO
;    TITLE OF INVENTION:  THE NEUROTROPHIC FACTOR NNT-1
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC.
;      STREET:  ONE AMGEN CENTER
;      CITY:  THOUSAND OAKS
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,534
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/792,019
;      FILING DATE:  03-FEB-1997
[redacted]
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOK, ROBERT R.
;      REGISTRATION NUMBER:  31,602
;      REFERENCE/DOCKET NUMBER:  A-442B
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  225 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-016-534-5

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  Best Local Similarity   96.7%;  Pred. No. 1.1e-118;
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Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
           ||||||||||||||||||:|||||||||:||||||||||||||||||||||||||||||||
Db      71 EPDFNPPRLGAETLPRATVNLEVWRSLNDRLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
           |||||||||||||||||||| |||||||||||||| | ||||||||||||||||||||||
Db     131 RSLAHFCTSLQGLLGSIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQKMDDFWLLKE 190

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
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Db     191 LQTWLWRSAKDFNRLKKKMQPPAASVTLHLEAHGF 225


RESULT 8
US-09-106-182-3
; Sequence 3, Application US/09106182
; Patent No. 6046035
;  GENERAL INFORMATION:
;    APPLICANT:  Shi, Yanggu
;    APPLICANT:  Ruben, Steve
;    TITLE OF INVENTION:  Cardiotrophin-Like Cytokine
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc
;      STREET:  9410 Key West Ave
;      CITY:  Rockville
;      STATE:  MD
;      COUNTRY:  US
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/106,182
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/051,053
;      FILING DATE:  30-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brookes, A. Anders
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PF385
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-309-8504
;      TELEFAX:  301-309-8439
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  203 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-106-182-3

  Query Match             10.7%;  Score 124.5;  DB 3;  Length 203;
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; Sequence 3, Application US/08233609
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;       COUNTRY:  USA
;       ZIP:  91320
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/016,534
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/792,019
;       FILING DATE:  03-FEB-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  COOK, ROBERT R.
;       REGISTRATION NUMBER:  31,602
;       REFERENCE/DOCKET NUMBER:  A-442B
;     INFORMATION FOR SEQ ID NO:  2:
;       SEQUENCE CHARACTERISTICS:
;       LENGTH:  225 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-016-534-2

  Query Match             100.0%;  Score 1169;  DB 4;  Length 225;
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  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
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Db      71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
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Db     191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225


RESULT 5
US-08-792-019B-5
; Sequence 5, Application US/08792019B
; Patent No. 5741772
;  GENERAL INFORMATION:
;    APPLICANT:  CHANG, MING-SHI
;    TITLE OF INVENTION:  THE NEUROTROPHIC FACTOR NNT-1
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC.
;      STREET:  1840 DEHAVILLAND DRIVE
;      CITY:  THOUSAND OAKS
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/792,019B
;      FILING DATE:  03-FEB-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOK, ROBERT R.
;      REGISTRATION NUMBER:  31,602
;      REFERENCE/DOCKET NUMBER:  A-442
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  225 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-792-019B-5

  Query Match             97.2%;  Score 1136;  DB 1;  Length 225;
  Best Local Similarity   96.7%;  Pred. No. 1.1e-118;
  Matches  208;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
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Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
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Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
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RESULT 6
US-08-988-819-5
; Sequence 5, Application US/08988819
; Patent No. 6054294
;  GENERAL INFORMATION:
;    APPLICANT:  CHANG, MING-SHI
;    TITLE OF INVENTION:  NEUROTROPHIC FACTOR NNT-1
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC.
;      STREET:  ONE AMGEN CENTER DRIVE
;      CITY:  THOUSAND OAKS
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/988,819
;      FILING DATE:  12-DEC-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/792,019
;      FILING DATE:  03-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOK, ROBERT R.
;      REGISTRATION NUMBER:  31,602
;      REFERENCE/DOCKET NUMBER:  A-442A
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  225 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-988-819-5

  Query Match             97.2%;  Score 1136;  DB 3;  Length 225;
  Best Local Similarity   96.7%;  Pred. No. 1.1e-118;
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Db    131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy    181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
          |||||||||||||||||||||||||||||||||||
Db    191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225


RESULT 2
US-09-106-182-2
; Sequence 2, Application US/09106182
; Patent No. 6046035
;  GENERAL INFORMATION:
;    APPLICANT:  Shi, Yanggu
;    APPLICANT:  Ruben, Steve
;    TITLE OF INVENTION:  Cardiotrophin-Like Cytokine
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc
;      STREET:  9410 Key West Ave
;      CITY:  Rockville
;      STATE:  MD
;      COUNTRY:  US
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/106,182
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/051,053
;      FILING DATE:  30-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brookes, A. Anders
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PF385
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-309-8504
;      TELEFAX:  301-309-8439
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  225 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-106-182-2

  Query Match             100.0%;  Score 1169;  DB 3;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-122;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
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Db     11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy     61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy    121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy    181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
          |||||||||||||||||||||||||||||||||||
Db    191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225


RESULT 3
US-08-988-819-2
; Sequence 2, Application US/08988819
; Patent No. 6054294
;  GENERAL INFORMATION:
;    APPLICANT:  CHANG, MING-SHI
;    TITLE OF INVENTION:  NEUROTROPHIC FACTOR NNT-1
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC.
;      STREET:  ONE AMGEN CENTER DRIVE
;      CITY:  THOUSAND OAKS
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/988,819
;      FILING DATE:  12-DEC-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/792,019
;      FILING DATE:  03-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOK, ROBERT R.
;      REGISTRATION NUMBER:  31,602
;      REFERENCE/DOCKET NUMBER:  A-442A
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  225 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-988-819-2

  Query Match             100.0%;  Score 1169;  DB 3;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-122;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy     61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy    121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy    181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
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Db    191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225


RESULT 4
US-09-016-534-2
; Sequence 2, Application US/09016534
; Patent No. 6143874
;  GENERAL INFORMATION:
;    APPLICANT:  CHANG, MING-SHI
;    APPLICANT:  ELLIOTT, GARY S.
;    APPLICANT:  SARMIENTO, ULLA
;    APPLICANT:  SENALDI, GIORGIO
;    TITLE OF INVENTION:  THE NEUROTROPHIC FACTOR NNT-1
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC.
;      STREET:  ONE AMGEN CENTER
;      CITY:  THOUSAND OAKS
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 13, 2003, 11:47:42 ; Search time 8.6 Seconds
(without alignments)
735.573 Million cell updates/sec

Title: US-09-521-335-2
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Sequence: 1 MLACLCTVLWHLPAVPALNR.....KKKMQPPAAAVTLHLGAHGF 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1169	100.0	225	3	US-08-988-819-2	Sequence 2, Appli
4	1169	100.0	225	4	US-09-016-534-2	Sequence 2, Appli
5	1136	97.2	225	1	US-08-792-019B-5	Sequence 5, Appli
6	1136	97.2	225	3	US-08-988-819-5	Sequence 5, Appli
7	1136	97.2	225	4	US-09-016-534-5	Sequence 5, Appli
8	124.5	10.7	203	3	US-09-106-182-3	Sequence 3, Appli
9	118.5	10.1	203	1	US-08-233-609-3	Sequence 3, Appli
10	118.5	10.1	203	1	US-08-444-083-3	Sequence 3, Appli
11	118.5	10.1	203	1	US-08-286-304-3	Sequence 3, Appli
12	118.5	10.1	203	1	US-08-442-745-3	Sequence 3, Appli
13	118.5	10.1	203	1	US-08-443-129-3	Sequence 3, Appli
14	118.5	10.1	203	1	US-08-443-952-3	Sequence 3, Appli
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ALIGNMENTS

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RESULT 1
US-08-792-019B-2
; Sequence 2, Application US/08792019B
; Patent No. 5741772
;  GENERAL INFORMATION:
;    APPLICANT:  CHANG, MING-SHI
;    TITLE OF INVENTION:  THE NEUROTROPHIC FACTOR NNT-1
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AMGEN INC.
;      STREET:  1840 DEHAVILLAND DRIVE
;      CITY:  THOUSAND OAKS
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  91320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/792,019B
;      FILING DATE:  03-FEB-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOK, ROBERT R.
;      REGISTRATION NUMBER:  31,602
;      REFERENCE/DOCKET NUMBER:  A-442
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  225 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-792-019B-2

  Query Match           100.0%;  Score 1169;  DB 1;  Length 225;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-122;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
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Db      11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
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Db      71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
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  Query Match             97.2%;  Score 1136;  DB 19;  Length 225;
  Best Local Similarity   96.7%;  Pred. No. 1.5e-111;
  Matches  208;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
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Db     131 RSLAHFCTSLQGLLGSIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQKMDDFWLLKE 190

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Db     191 LQTWLWRSAKDFNRLKKKMQPPAASVTLHLEAHGF 225


[redacted]LT 15
A[redacted]36142
ID   AAW56142 standard; Protein; 225 AA.
XX
AC   AAW56142;
XX
DT   13-JUL-1998  (first entry)
XX
DE   Amino acid sequence of murine neurotrophic factor NNT-1.
XX
KW   Mouse; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
KW   treatment; neurological disease; degeneration; Parkinson's disease;
KW   amyotropic lateral sclerosis; ALS; Alzheimers's disease; stroke.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /note= "signal peptide"
FT   Protein         28..225
FT                   /note= "mature peptide"
XX
PN   US5741772-A.
XX
PD   21-APR-1998.
XX
PF   03-FEB-1997;   97US-0792019.
XX
[redacted]  03-FEB-1997;   97US-0792019.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Chang M;
XX
DR   WPI; 1998-260526/23.
DR   N-PSDB; AAV22654.
XX
PT   Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
PT   useful for stimulating growth of motor and sympathetic neurons
XX
PS   Claim 2; Fig 5; 41pp; English.
XX
CC   The present sequence represents a murine neurotrophic factor, designated
CC   NNT-1, which is capable of stimulating growth of motor or sympathetic
CC   neurons. The NNT-1 protein is useful in the treatment of neurological
CC   diseases characterised by the degeneration and death of particular
CC   classes of neurons. These diseases specifically include Parkinson's
CC   disease, amyotropic lateral sclerosis (ALS), Alzheimers's disease,
CC   stroke and various degenerative disorders affecting vision.
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SQ   Sequence   225 AA;
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  Query Match             97.2%;  Score 1136;  DB 19;  Length 225;
  Best Local Similarity   96.7%;  Pred. No. 1.5e-111;
  Matches  208;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
           |||||||||||||||||:|||||||||:|||||||||||||||||||||||||||||||||
Db      71 EPDFNPPRLGAETLPRATVNLEVWRSLNDRLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
           |||||||||||||||||||| |||||||||||||| | ||||||||||||||||||||||
Db     131 RSLAHFCTSLQGLLGSIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQKMDDFWLLKE 190

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
           |||||||||||||||||||||:||||| ||||
Db     191 LQTWLWRSAKDFNRLKKKMQPPAASVTLHLEAHGF 225
```


Search completed: March 13, 2003, 11:49:17
Job time : 23.704 secs

XX
DE Mouse interleukin-B60 (IL-B60).
XX
KW Interleukin-B60; IL-B60; mouse; cytokine; cytokine-like factor-1;
KW haematopoietic; inflammation; antiinflammatory; autoimmune disease;
KW therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= Signal_peptide
FT Protein 18..215
FT /label= Mature-protein
XX
PN WO200053631-A1.
XX
PD 14-SEP-2000.
XX
[redacted] 09-MAR-2000; 2000WO-US06182.
XX
PR 11-MAR-1999; 99US-0267901.
XX
PA (SCHE) SCHERING CORP.
XX
PI Oppmann B, Timans JC; Kastelein RA, Bazan JF;
XX
DR WPI; 2000-587426/55.
DR N-PSDB; AAA88547.
XX
PT Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
PT polypeptides, and nucleic acids, useful in research, diagnosis and for
PT treating inflammatory and autoimmune disorders -
XX
PS Claim 1; Page 17; 97pp; English.
XX
CC The present sequence is that of mouse interleukin-B60 (IL-B60), a
CC novel, small soluble cytokine-like protein that exhibits structural
CC motifs characteristic of a member of the long-chain cytokines, and
CC which shows homology to granulocyte colony stimulating factor and
CC interleukin-6. IL-60B may have either stimulatory or inhibitory
CC effects on haematopoietic cells, including e.g. lymphoid cells,
CC such as T-cells, B-cells, natural killer cells, macrophages,
CC dendritic cells, haematopoietic progenitors, etc. Methods are
CC provided for modulating the physiology or development of a cell or
CC tissue culture cells by contacting the cell with an agonist or
CC [redacted] antagonist of IL-B60 or an agonist of antagonist of a complex of
CC [redacted] mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see
CC [redacted] AAB19588). The IL-B60/CLF-1 cytokine serves as a key physiological
CC factor in motor neuron development and regeneration. IL-60B, its
CC agonists and antagonists may be used to treat inflammatory or
CC autoimmune disorders and also for drug screening.
XX
SQ Sequence 215 AA;

Query Match 97.2%; Score 1136; DB 21; Length 215;
Best Local Similarity 96.7%; Pred. No. 1.4e-111;
Matches 208; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
          |||||||||||||||||:|||||||||:|||||||||||||||||||||||||||||||||
Db      61 EPDFNPPRLGAETLPRATVNLEVWRSLNDRLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
          |||||||||||||||||||| |||||||||||||| | ||||||||||||||||||||||||
Db     121 RSLAHFCTSLQGLLGSIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQKMDDFWLLKE 180

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
          |||||||||||||||||||||||:||||| ||||
Db     181 LQTWLWRSAKDFNRLKKKMQPPAASVTLHLEAHGF 215
```

RESULT 14
AAW29716
ID AAW29716 standard; Protein; 225 AA.
XX
AC AAW29716;
XX
DT 09-NOV-1998 (first entry)
XX
DE Mouse neurotrophic factor NNT-1.
XX
KW NNT-1; neurotrophic factor; mouse; antiinflammatory; adjuvant;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW peripheral neurophathy; dystrophy; neural retina degeneration;
KW common variable immunodeficiency; CVID; selective IgA deficiency;
KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
KW therapy.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT /label= Sig_peptide
FT Protein 28..225
FT /label= Mat_protein
XX
PN WO9833922-A1.
XX
PD 06-AUG-1998.
XX
PF 02-FEB-1998; 98WO-US02363.
XX
PR 30-JAN-1998; 98US-0016534.
PR 03-FEB-1997; 97US-0792019.
XX
PA (AMGE-) AMGEN INC.
XX
PI Chang M, Elliot GS, Sarmiento U, Senaldi G;
XX
DR WPI; 1998-437475/37.
DR N-PSDB; AAV47512.
XX
PT Newly isolated nucleic acid encoding human or murine neurotrophic
PT factor NNT-1 - useful for treatment of neurological and
PT immunological diseases or inflammation, also as vaccine adjuvant
XX
PS Claim 13; Fig 5; 120pp; English.
XX
CC This is the amino acid sequence of a murine neurotrophic factor,
CC designated NNT-1, that is a growth factor for neurons and for B or
CC T cells. It was deduced from isolated NNT-1 cDNA (see AAV47512).
CC Human NNT-1 (see AAW29715) is also provided. Vectors and host cells
CC for use in the production of human murine recombinant NNT-1
CC polypeptides. These are used to treat: (i) neurological or
CC immunological diseases, specifically Alzheimer's, Parkinson's
CC or Huntington's diseases, amyotrophic lateral sclerosis,
CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
CC degeneration of the neural retina, or conditions characterised by T
CC or B cell defects, e.g. common variable immunodeficiency (CVID),
CC selective IgA deficiency, hypogammaglobulinaemia and X-linked
CC agammaglobulinaemia (claimed), but many others disclosed; and (ii)
CC inflammation. NNT-1 is also able to boost immunoreactivity and
CC antibody production following vaccination, and, since it inhibits
CC tumour necrosis factor production, it may also be useful for
CC treating sepsis. In addition, cells that have been engineered to
CC express NNT-1 can be implanted, or nucleic acids are delivered in
CC gene therapy vectors.
XX
SQ Sequence 225 AA;

```
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   N-PSDB; AAK51548.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 20; Page 3306; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence   260 AA;

  Query Match             99.4%;  Score 1162;  DB 22;  Length 260;
  Best Local Similarity   99.5%;  Pred. No. 3.3e-114;
  Matches  214;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db      46 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDPTRYLEHQLRSLAGTYLNYLGPPFN 105

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     106 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 165

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     166 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 225

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
           |||||||||||||||||||||||||||||||||||
Db     226 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 260


RESULT 12
AAE00828
ID   AAE00828 standard; Protein; 223 AA.
XX
AC   AAE00828;
XX
DT   02-JUL-2001  (first entry)
XX
DE   Human cardiotrophin-like cytokine (CLC) protein.
XX
KW   Human; biologically active complex; haemopoietin receptor; NR6;
KW   cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
KW   differentiation; cell survival; neurotrophic activity.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /label= Signal_peptide
FT   Protein         28..223
FT                   /label= Human_mature_CLC_protein
FT                   /note= "Cardiotrophin-like cytokine"
XX
PN   WO200127157-A1.
XX
PD   19-APR-2001.
XX
PF   06-OCT-2000; 2000WO-AU01216.
XX
PR   08-OCT-1999;   99AU-0003327.
PR   12-MAY-2000; 2000AU-0007489.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Nash A,  Jachno KM,  Fabri LJ,  Reid K,  Bartlett PF,  Hilton DJ;
PI   Nakata Y,  Hasegawa M;
XX
DR   WPI; 2001-281978/29.
DR   N-PSDB; AAD04201.
XX
PT   New biologically active complex comprising NR6 and
PT   cardiotrophin-like-cytokine, for facilitating proliferation,
PT   differentiation and/or survival of a cell -
XX
PS   Claim 32; Page 114-115; 123pp; English.
XX
CC   The present invention relates to a biologically active complex comprising
CC   a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC).
CC   The complex is useful in the manufacture of a medicament for the
CC   treatment and/or prophylaxis of a subject, as it is involved in
CC   facilitating proliferation, differentiation and/or survival of a cell.
CC   The complex or its components have neurotrophic activity. The present
CC   sequence is human cardiotrophin-like cytokine (CLC) protein.
XX
SQ   Sequence   223 AA;

  Query Match             99.0%;  Score 1157;  DB 22;  Length 223;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-114;
  Matches  213;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAH 213
           |||||||||||||||||||||||||||||||||
Db     191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAH 223


RESULT 13
AAB19587
ID   AAB19587 standard; Protein; 215 AA.
XX
AC   AAB19587;
XX
DT   22-JAN-2001  (first entry)
```

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention.
XX
SQ Sequence 321 AA;

ery Match 100.0%; Score 1169; DB 22; Length 321;
st Local Similarity 100.0%; Pred. No. 8.1e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
Db 107 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 166

Qy 61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
Db 167 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 226

Qy 121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Db 227 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 286

Qy 181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
Db 287 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 321

RESULT 10
AAM79399
ID AAM79399 standard; Protein; 321 AA.
XX
AC AAM79399;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3045.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK52532.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 237; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 321 AA;

Query Match 100.0%; Score 1169; DB 22; Length 321;
Best Local Similarity 100.0%; Pred. No. 8.1e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
Db 107 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 166

Qy 61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
Db 167 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 226

Qy 121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Db 227 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 286

Qy 181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
Db 287 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 321

RESULT 11
AAM78415
ID AAM78415 standard; Protein; 260 AA.
XX
AC AAM78415;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1077.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.

KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder.
XX
OS Homo sapiens.
XX
PN WO200153455-A2.
XX
PD 26-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-US35017.
XX
PR 23-DEC-1999; 99US-0471275.
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457603/49.
DR N-PSDB; AAH99772.
XX
PT Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
PS Claim 20; Page 278; 1217pp; English.
XX
CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production, The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.
XX
SQ Sequence 253 AA;

Query Match 100.0%; Score 1169; DB 22; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.8e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 98

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      99 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 158

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     159 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 218

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
          |||||||||||||||||||||||||||||||||||
Db     219 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 253
```

RESULT 9
ABB11896
ID ABB11896 standard; peptide; 321 AA.
XX
AC ABB11896;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human cardiotrophin-like cytokine homologue, SEQ ID NO:2266.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR N-PSDB; ABA09140.
XX
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
PS Claim 20; Page 273; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell

CC inhibit differentiation of cells stocks. The complex is also used to
CC modulate activity of the gp130/LIFRbeta receptor or cells expressing
CC that receptor, particularly those cells implicated in the immune,
CC haematopoietic, nervous or reproductive system, the liver or skeletal
CC muscle. Molecules of the invention may be used to prevent or treat
CC neurodegenerative diseases including amyotrophic lateral sclerosis,
CC Parkinson's and Huntington's disease, to repair or regenerate nervous
CC or muscular tissue or to maintain muscular mass in paralysis patients.
CC They may also be used to treat cancer, obesity and associated diseases,
CC and to improve fertility, particularly to avoid endometriosis and/or
CC assist blastocyst implantation, thrombosis, or retinal disease,
CC particular retinal pigmentosis.
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 1169; DB 22; Length 225;
Best Local Similarity 100.0%; Pred. No. 5e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
Db 11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy 61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
Db 71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy 121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy 181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
Db 191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225

RESULT 7
AAU78176
ID AAU78176 standard; Protein; 225 AA.
XX
AC AAU78176;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human novel neurotrophic factor NNT1.
XX
KW Human; NNT1; neurotrophic factor; IgE-related disease;
KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
KW vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
KW inflammatory bowel disease; transplant rejection; reproductive disorder;
KW graft versus host disease; infertility; miscarriage; preterm labour.
XX
OS Homo sapiens.
XX
PN WO200215977-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US25906.
XX
PR 18-AUG-2000; 2000US-226436P.
PR 16-AUG-2001; 2001US-0931704.
XX
PA (AMGE-) AMGEN INC.
XX
PI Senaldi G;
XX
DR WPI; 2002-280867/32.
DR N-PSDB; ABK11647.
XX
PT Treating Immunoglobulin E-related disease, modulating IgE levels in a
PT patient, preventing IgE-related disease and treating allergic diseases,
PT involves administering NNT-1 inhibitor to a patient -
XX
PS Claim 2; Fig 3; 63pp; English.
XX
CC The invention relates to treating Immunoglobulin E (IgE)-related disease,
CC modulating IgE levels in a patient, preventing an IgE-related disease,
CC and treating allergic diseases, comprising administering a
CC therapeutically effective amount of novel neurotrophic factor (NNT)-1
CC inhibitor to a patient. Also included are a method of diagnosing an
CC IgE-related disease or susceptibility to an IgE-related disease, by
CC determining the presence or amount of expression of an NNT1 polypeptide
CC encoded by a NNT1 nucleotide sequence, its fragment or naturally
CC occurring variant, and diagnosing an IgE-related disease or
CC susceptibility of an IgE-related disease based on the presence or amount
CC of expression of the polypeptide and a pharmaceutical composition for use
CC in treating IgE-related disease, comprising the NNT1 inhibitor.
CC The NNT1 inhibitor is useful for preventing and treating IgE-related
CC disease, modulating IgE levels, and treating allergic diseases e.g.
CC Type I allergic disease, allergic rhinitis, eczema, dermatitis,
CC pollinosis, asthma, immune diseases and disorders, diseases involving
CC abnormal cell proliferation including cancer, arteriosclerosis and
CC vascular restenosis, diseases and conditions relating to dysfunction of
CC immune system including rheumatoid arthritis, psoriatic arthritis,
CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,
CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory
CC bowel disease, transplant rejection, and graft versus host disease, and
CC reproductive diseases and disorders including infertility, miscarriage,
CC preterm labour and delivery, and endometriosis. The present sequence
CC represents human NNT1.
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 1169; DB 23; Length 225;
Best Local Similarity 100.0%; Pred. No. 5e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
Db 11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy 61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
Db 71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy 121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy 181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
Db 191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225

RESULT 8
AAM25831
ID AAM25831 standard; Protein; 253 AA.
XX
AC AAM25831;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:1346.
XX
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;

```
Qy    121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy    181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
          |||||||||||||||||||||||||||||||||||
Db    191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225


RESULT 5
AAY87813
ID   AAY87813 standard; Protein; 225 AA.
XX
AC   AAY87813;
XX
DT   24-AUG-2000  (first entry)
XX
DE   Human NNT-1 protein.
XX
KW   NNT-1; human; neurotrophic factor; nootropic; neuroprotective; treatment;
KW   anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
KW   nervous system degeneration; Alzheimer's disease; Parkinson's disease;
KW   amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW   Huntington's disease; peripheral neuropathy; neural retina degeneration;
KW   retinopathy; immune disorder; hematopoietic disorder.
XX
OS   Homo sapiens.
XX
PN   US6054294-A.
XX
PD   25-APR-2000.
XX
PF   12-DEC-1997;   97US-0988819.
XX
PR   03-FEB-1997;   97US-0792019.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Chang M;
XX
DR   WPI; 2000-338492/29.
DR   N-PSDB; AAA39481.
XX
PT   New nucleic acids encoding neurotrophic factors useful for stimulating
PT   growth of motor or sympathetic neurons for treating neuron cell damage
PT   -
XX
PS   Claim 1c; Fig 3; 42pp; English.
XX
CC   This invention describes a novel nucleic acid molecule (I) encoding a
CC   novel neurotrophic factor (NNT-1) (II) which has nootropic,
CC   neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
CC   ophthalmological activity. (I) is useful for producing NNT-1
CC   polypeptides which are useful for treating patients in whom various
CC   cells of the central, autonomic, or peripheral nervous system have
CC   degenerated and/or have been damaged by congenital disease, trauma,
CC   mechanical damage, surgery, stroke, ischemia, infection, metabolic
CC   disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
CC   proteins are used to treat diseases like Alzheimer's, Parkinson's,
CC   amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
CC   disease, peripheral neuropathy induced by diabetes or other metabolic
CC   disorders, and/or dystrophies or degeneration of the neural retina such
CC   as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
CC   night blindness, progressive cone-rod degeneration, immune disorders and
CC   hematopoietic disorders. (I) is effective in treating neurological
CC   conditions and promotes neuron regeneration. Neural functions are
CC   effectively restored in patients suffering from various neurological
CC   disorders. This sequence represents the human NNT-1 protein described in
CC   the method of the invention.
XX
SQ   Sequence   225 AA;

  Query Match             100.0%;  Score 1169;  DB 21;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 5e-115;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy     61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy    121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy    181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
          |||||||||||||||||||||||||||||||||||
Db    191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225


RESULT 6
AAG63543
ID   AAG63543 standard; Protein; 225 AA.
XX
AC   AAG63543;
XX
DT   15-OCT-2001  (first entry)
XX
DE   Amino acid sequence of a human NNT-1 protein.
XX
KW   NNT-1; CLF-1; sCNTFRalpha; nervous system; neuron; nervous system;
KW   neuro-muscular function; tumour; immune system; haematopoietic system;
KW   reproductive system; liver; skeletal muscle; neurodegenerative disease;
KW   amyotrophic lateral sclerosis; Parkinson's disease; Huntingdon's disease;
KW   muscular mass; paralysis; cancer; obesity; fertility; endometriosis;
KW   blastocyst implantation; thrombosis; retinal disease;
KW   retinal pigmentosis.
XX
OS   Homo sapiens.
XX
PN   WO200155172-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001; 2001WO-FR00253.
XX
PR   27-JAN-2000; 2000FR-0001035.
PR   12-OCT-2000; 2000FR-0013089.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI   Elson G,  Gauchat J,  Plun-Favreau H,  Chevalier S,  Gascan H;
XX
DR   WPI; 2001-488773/53.
DR   N-PSDB; AAH74484.
XX
PT   A complex comprising a NNT-1 protein and a CLF-1 and/or sCNTFRalpha
PT   protein useful to treat neurodegenerative disease including Parkinson's
PT   and Huntington's, obesity and cancer  -
XX
PS   Claim 2; Page 58; 67pp; French.
XX
CC   The present sequence represents a human NNT-1 protein. The specification
CC   describes a complex comprising a NNT-1 protein and a CLF-1 and/or
CC   sCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate
CC   activity of the sCNTFRalpha/gp130/LIFRbeta receptor complex, or to
CC   induce phosphorylation of the tyrosine of gp130 and LIFRbeta,
CC   particularly where cells expressing the receptor complex are in the
CC   central or peripheral nervous system, in neurons implicated in
CC   neuro-muscular function or in skeletal muscle. The complex or
CC   antibodies are also used to decrease the survival, growth or
CC   proliferation of tumour cells or to facilitate the proliferation and/or
```

```
XX
DT   13-JUL-1998  (first entry)
XX
DE   Amino acid sequence of human neurotrophic factor NNT-1.
XX
KW   Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
KW   treatment; neurological disease; degeneration; Parkinson's disease;
KW   amyotropic lateral sclerosis; ALS; Alzheimers's disease; stroke.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /note= "signal peptide"
FT   Protein         28..225
FT                   /note= "mature protein"
XX
PN   US5741772-A.
XX
[redacted]21-APR-1998.
XX
PF   03-FEB-1997;   97US-0792019.
XX
PR   03-FEB-1997;   97US-0792019.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Chang M;
XX
DR   WPI; 1998-260526/23.
DR   N-PSDB; AAV22652.
XX
PT   Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
PT   useful for stimulating growth of motor and sympathetic neurons
XX
PS   Claim 1; Fig 3; 41pp; English.
XX
CC   The present sequence represents a human neurotrophic factor, designated
CC   NNT-1, which is capable of stimulating growth of motor or sympathetic
CC   neurons. The NNT-1 protein is useful in the treatment of neurological
CC   diseases characterised by the degeneration and death of particular
CC   classes of neurons. These diseases specifically include Parkinson's
CC   disease, amyotropic lateral sclerosis (ALS), Alzheimers's disease,
CC   stroke and various degenerative disorders affecting vision.
XX
SQ   Sequence   225 AA;

[redacted]ery Match            100.0%;  Score 1169;  DB 19;  Length 225;
[redacted]st Local Similarity   100.0%;  Pred. No. 5e-115;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
           |||||||||||||||||||||||||||||||||||
Db     191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225


RESULT 4
AAW94466
ID   AAW94466 standard; Protein; 225 AA.
XX
AC   AAW94466;
XX
DT   22-APR-1999  (first entry)
XX
DE   Human cardiotrophin-like cytokine protein.
XX
KW   Human; cardiotrophin-like cytokine; interleukin 6 cytokine family;
KW   CLC; IL-6; diagnosis; detection; immune system-related disorder;
KW   cancer; cardiac disorder; heart failure; hypertension; cancer;
KW   autoimmune disorder; infection.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /label= signal
FT   Protein         28..225
FT                   /label= Cardiotrophin-like_cytokine
FT   Domain          74..79
FT                   /label= CD-I
FT                   /note= "conserved domain"
FT   Domain          150..156
FT                   /label= CD-II
FT                   /note= "conserved domain"
FT   Domain          194..198
FT                   /label= CD-III
FT                   /note= "conserved domain"
XX
PN   WO9900415-A1.
XX
PD   07-JAN-1999.
XX
PF   29-JUN-1998;   98WO-US13129.
XX
PR   30-JUN-1997;   97US-0051311.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Shi Y;
XX
DR   WPI; 1999-095678/08.
DR   N-PSDB; AAX16161.
XX
PT   New isolated cardiotrophin-like cytokine nucleic acid - used to
PT   develop products for treating cardiac and immune system disorders,
PT   e.g. heart failure, hypertension, cancers, autoimmune disorders and
PT   infections
XX
PS   Claim 1; Fig 1; 103pp; English.
XX
CC   The present invention relates to a novel cardiotrophin-like cytokine
CC   (CLC) protein which is a member of the interleukin 6 (IL-6) cytokine
CC   family. The present sequence represents the human CLC protein. The
CC   present invention also describes screening methods for identifying
CC   agonists and antagonists of CLC activity, as well as methods for
CC   detecting cardiac and immune system-related disorders and
CC   therapeutic methods for treating cardiac and immune system-related
CC   disorders, e.g heart failure, hypertension, cancers, autoimmune
CC   disorders and infections.
XX
SQ   Sequence   225 AA;

  Query Match            100.0%;  Score 1169;  DB 20;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 5e-115;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130
```

```
XX
DR   WPI; 2000-587426/55.
DR   N-PSDB; AAA88546.
XX
PT   Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
PT   polypeptides, and nucleic acids, useful in research, diagnosis and for
PT   treating inflammatory and autoimmune disorders -
XX
PS   Claim 1; Page 15-16; 97pp; English.
XX
CC   The present sequence is that of human interleukin-B60 (IL-B60), a
CC   novel, small soluble cytokine-like protein that exhibits structural
CC   motifs characteristic of a member of the long-chain cytokines, and
CC   which shows homology to granulocyte colony stimulating factor and
CC   interleukin-6.  IL-60B may have either stimulatory or inhibitory
CC   effects on haematopoietic cells, including e.g. lymphoid cells,
CC   such as T-cells, B-cells, natural killer cells, macrophages,
CC   dendritic cells, haematopoietic progenitors, etc.  Methods are
CC   provided for modulating the physiology or development of a cell or
CC   tissue culture cells by contacting the cell with an agonist or
CC   antagonist of IL-B60 or an agonist of antagonist of a complex of
CC   mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see
CC   AAB19588).  The IL-B60/CLF-1 cytokine serves as a key physiological
CC   factor in motor neuron development and regeneration.  IL-60B, its
CC   agonists and antagonists may be used to treat inflammatory or
CC   autoimmune disorders and also for drug screening.
XX
SQ   Sequence   215 AA;

  Query Match             100.0%;  Score 1169;  DB 21;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-115;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
          |||||||||||||||||||||||||||||||||||||
Db     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215


RESULT 2
AAW29715
ID   AAW29715 standard; Protein; 225 AA.
XX
AC   AAW29715;
XX
DT   09-NOV-1998  (first entry)
XX
DE   Human neurotrophic factor NNT-1.
XX
KW   NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
KW   Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW   amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW   peripheral neuropathy; dystrophy; neural retina degeneration;
KW   common variable immunodeficiency; CVID; selective IgA deficiency;
KW   hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
KW   therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..27
FT                   /label= Sig_peptide
FT   Protein         28..225
FT                   /label= Mat_protein
XX
PN   WO9833922-A1.
XX
PD   06-AUG-1998.
XX
PF   02-FEB-1998;   98WO-US02363.
XX
PR   30-JAN-1998;   98US-0016534.
PR   03-FEB-1997;   97US-0792019.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Chang M,  Elliot GS,  Sarmiento U,  Senaldi G;
XX
DR   WPI; 1998-437475/37.
DR   N-PSDB; AAV47510-11.
XX
PT   Newly isolated nucleic acid encoding human or murine neurotrophic
PT   factor NNT-1 - useful for treatment of neurological and
PT   immunological diseases or inflammation, also as vaccine adjuvant
XX
PS   Claim 12; Fig 3; 120pp; English.
XX
CC   This is the amino acid sequence of a novel neurotrophic factor,
CC   designated NNT-1, that is a growth factor for neurons and for B or
CC   T cells.  It was deduced from isolated cDNA (see AAV47510) and
CC   genomic DNA (see AAV47511) clones.  Vectors containing the cDNA or
CC   genomic DNA and host cells are provided for use in the production
CC   of NNT-1 polypeptides.  These are used to treat: (i) neurological
CC   or immunological diseases, specifically Alzheimer's, Parkinson's
CC   or Huntington's diseases, amyotrophic lateral sclerosis,
CC   Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
CC   degeneration of the neural retina, or conditions characterised by T
CC   or B cell defects, e.g. common variable immunodeficiency (CVID),
CC   selective IgA deficiency, hypogammaglobulinaemia and X-linked
CC   agammaglobulinaemia (claimed), but many others disclosed; and (ii)
CC   inflammation.  NNT-1 is also able to boost immunoreactivity and
CC   antibody production following vaccination, and, since it inhibits
CC   tumour necrosis factor production, it may also be useful for
CC   treating sepsis.  In addition, cells that have been engineered to
CC   express NNT-1 can be implanted, or nucleic acids are delivered in
CC   gene therapy vectors.
XX
SQ   Sequence   225 AA;

  Query Match             100.0%;  Score 1169;  DB 19;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 5e-115;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

Qy      61 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 EPDFNPPRLGAETLPRATVDLEVWRSLNDKLRLTQNYEAYSHLLCYLRGLNRQAATAELR 130

Qy     121 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 RSLAHFCTSLQGLLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy     181 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 215
          |||||||||||||||||||||||||||||||||||||
Db     191 LQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF 225


RESULT 3
AAW56141
ID   AAW56141 standard; Protein; 225 AA.
XX
AC   AAW56141;
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 13, 2003, 11:41:12 ; Search time 22.704 Seconds
(without alignments)
1261.843 Million cell updates/sec

Title: US-09-521-335-2
Perfect score: 1169
Sequence: 1 MLACLCTVLWHLPAVPALNR.....KKKMQPPAAAVTLHLGAHGF 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1169	100.0	215	21	AAB19586	Human interleukin-
2	1169	100.0	225	19	AAW29715	Human neurotrophic
3	1169	100.0	225	19	AAW56141	Amino acid sequenc
4	1169	100.0	225	20	AAW94466	Human cardiotrophi
5	1169	100.0	225	21	AAY87813	Human NNT-1 protei
6	1169	100.0	225	22	AAG63543	Amino acid sequenc
7	1169	100.0	225	23	AAU78176	Human novel neurot
8	1169	100.0	253	22	AAM25831	Human protein sequ
9	1169	100.0	321	22	ABB11896	Human cardiotrophi
10	1169	100.0	321	22	AAM79399	Human protein SEQ
11	1162	99.4	260	22	AAM78415	Human protein SEQ
12	1157	99.0	223	22	AAE00828	Human cardiotrophi
13	1136	97.2	215	21	AAB19587	Mouse interleukin-
14	1136	97.2	225	19	AAW29716	Mouse neurotrophic
15	1136	97.2	225	19	AAW56142	Amino acid sequenc
16	1136	97.2	225	21	AAY87814	Murine NNT-1 prote
17	1136	97.2	225	23	AAU78177	Mouse novel neurot
18	885	75.7	164	22	ABB40317	Peptide #7823 enco
19	885	75.7	164	22	ABB24716	Protein #6715 enco
20	885	75.7	164	22	AAM61118	Human brain expres
21	885	75.7	164	22	AAM73827	Human bone marrow
22	885	75.7	164	22	AAM20115	Peptide #6549 enco
23	885	75.7	164	22	AAM34012	Peptide #8049 enco
24	885	75.7	164	23	ABG43716	Human peptide enco
25	162.5	13.9	208	20	AAY09197	Human DNAX interle
26	160	13.7	208	20	AAY09196	Human DNAX interle
27	118.5	10.1	203	16	AAR83965	Mouse cardiac hype
28	118.5	10.1	203	17	AAR88204	Human cardiotrophi
29	118.5	10.1	203	18	AAW29237	Murine cardiotroph
30	92	7.9	332	21	AAG22132	Arabidopsis thalia
31	92	7.9	332	21	AAG40321	Arabidopsis thalia
32	91.5	7.8	201	16	AAR83967	Human cardiac hype
33	91.5	7.8	201	18	AAW29238	Human cardiotrophi
34	91.5	7.8	201	20	AAY06490	Human tumour-assoc
35	91.5	7.8	201	21	AAB27662	Human protein PRO8
36	91.5	7.8	201	21	AAB13004	Human cardiotrophi
37	91.5	7.8	201	21	AAY93697	Amino acid sequenc
38	91.5	7.8	201	21	AAY87818	Human cardiotrophi
39	91.5	7.8	201	22	AAB50994	Human PRO882 prote
40	91	7.8	195	14	AAR34432	Sequence of growth
41	91	7.8	195	20	AAW83337	Chicken ciliary ne
42	91	7.8	1182	23	AAE19798	Mouse Hairless pro
43	90	7.7	232	22	AAU09152	Human cytokine Zal
44	90	7.7	232	23	AAU76374	Human helical prot
45	90	7.7	242	22	AAB20275	Human interleukin

ALIGNMENTS

RESULT 1
AAB19586
ID AAB19586 standard; Protein; 215 AA.
XX
AC AAB19586;
XX
DT 22-JAN-2001 (first entry)
XX
DE Human interleukin-B60 (IL-B60).
XX
KW Interleukin-B60; IL-B60; human; cytokine; cytokine-like factor-1;
KW haematopoietic; inflammation; antiinflammatory; autoimmune disease;
KW therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= Signal_peptide
FT Protein 18..215
FT /label= Mature-protein
XX
PN WO200053631-A1.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US06182.
XX
PR 11-MAR-1999; 99US-0267901.
XX
PA (SCHE) SCHERING CORP.
XX
PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;

```
RT   and colon cancer derived by splicing to exon 11.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF492470; AAM18048.1; -.
KW   Receptor.
SQ   SEQUENCE   268 AA;  30705 MW;  FBB498AB649A078C CRC64;

  Query Match             14.9%;  Score 333;  DB 4;  Length 268;
  Best Local Similarity   36.6%;  Pred. No. 3.2e-21;
  Matches   83;  Conservative   29;  Mismatches   97;  Indels   18;  Gaps    8;

Qy    123 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 181
          :   :||  | ||| ||    | | | :  || | ||  |   | ||||| |
Db     15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72

Qy    182 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
          : | :| | ||:|||  |   :::  | : | |||::||: || | :|:  :|  ||| :
Db     73 HECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLE 132

Qy    241 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 295
          : |  |   ||:    |:  ||| | |     |   |:|| : | : :|: :     ||
Db    133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTE 190

Qy    296 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSE 342
           ::  | ||  | ||||| |          | || ||  |    | :
Db    191 FKILSLHPGQKYLVQVRCKP-------DHGYWSAWSPATFIQIPSGD 230


RESULT 7
Q96P36
ID   Q96P36      PRELIMINARY;      PRT;   288 AA.
AC   Q96P36;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Prolactin receptor short isoform A.
GN   PRLR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Trott J.F., Hovey R.C., Vonderhaar B.K.;
RT   "Expression of two novel hPRLR isoforms in breast tumors.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF416618; AAL23914.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003528; Hemtopoptn_L_F1.
DR   Pfam; PF00041; fn3; 2.
DR   PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW   Receptor.
SQ   SEQUENCE   288 AA;  32760 MW;  B45203EC045EB417 CRC64;

  Query Match             14.9%;  Score 332;  DB 4;  Length 288;
  Best Local Similarity   37.1%;  Pred. No. 4.3e-21;
  Matches   83;  Conservative   28;  Mismatches   95;  Indels   18;  Gaps    8;

Qy    123 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 181
          :   :||  | ||| ||    | | | :  || | ||  |   | ||||| |
Db     15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72

Qy    182 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
          : | :| | ||:|||  |   :::  | : | |||::||: || | :|:  :|  ||| :
Db     73 HECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLE 132

Qy    241 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 295
          : |  |   ||:    |:  ||| | |     |   |:|| : | : :|: :     ||
Db    133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTE 190

Qy    296 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 339
           ::  | ||  | ||||| |       . | || ||  |    |
Db    191 FKILSLHPGQKYLVQVRCKP-------DHGYWSAWSPATFIQIP 227


RESULT 8
Q9UHJ5
ID   Q9UHJ5      PRELIMINARY;      PRT;   349 AA.
AC   Q9UHJ5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Intermediate prolactin receptor isoform.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20054419; PubMed=10585417;
RA   Kline J.B., Roehrs H., Clevenger C.V.;
RT   "Functional characterization of the intermediate isoform of the human
RT   prolactin receptor.";
RL   J. Biol. Chem. 274:35461-35468(1999).
DR   EMBL; AF166329; AAD49855.1; -.
DR   HSSP; P16471; 1BP3.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003528; Hemtopoptn_L_F1.
DR   Pfam; PF00041; fn3; 2.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW   Receptor.
SQ   SEQUENCE   349 AA;  39806 MW;  932F200E850CDD27 CRC64;

  Query Match             14.9%;  Score 332;  DB 4;  Length 349;
  Best Local Similarity   37.1%;  Pred. No. 5.6e-21;
  Matches   83;  Conservative   28;  Mismatches   95;  Indels   18;  Gaps    8;

Qy    123 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 181
          :   :||  | ||| ||    | | | :  || | ||  |   | ||||| |
Db     15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72

Qy    182 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
          : | :| | ||:|||  |   :::  | : | |||::||: || | :|:  :|  ||| :
Db     73 HECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLE 132

Qy    241 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 295
          : |  |   ||:    |:  ||| | |     |   |:|| : | : :|: :     ||
Db    133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTE 190

Qy    296 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 339
           ::  | ||  | ||||| |          | || ||  |    |
Db    191 FKILSLHPGQKYLVQVRCKP-------DHGYWSAWSPATFIQIP 227


RESULT 9
Q96P35
ID   Q96P35      PRELIMINARY;      PRT;   376 AA.
AC   Q96P35;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Prolactin receptor short isoform B.
GN   PRLR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Trott J.F., Hovey R.C., Vonderhaar B.K.;
RT   "Expression of two novel hPRLR isoforms in breast tumors.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
```

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Db     301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE 360

Qy     358 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           ||||||||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 413


RESULT 4
Q9W6U9
ID   Q9W6U9      PRELIMINARY;      PRT;   918 AA.
AC   Q9W6U9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Glycoprotein 130 precursor.
GN   GP130.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYONIC HEART PRIMARY CULTURE;
RX   MEDLINE=99026068; PubMed=9806927;
RA   Geissen M., Heller S., Pennica D., Ernsberger U., Rohrer H.;
RT   "The specification of sympathetic neurotransmitter phenotype depends
RT   on gp130 cytokine receptor signaling.";
RL   Development 125:4791-4801(1998).
DR   EMBL; AJ011688; CAB42084.1; -.
DR   HSSP; P40189; 1BQU.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003529; Hemtopoptn_L_F2.
DR   Pfam; PF00041; fn3; 4.
DR   SMART; SM00060; FN3; 3.
DR   PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
KW   Signal.
FT   SIGNAL        1      26       POTENTIAL.
SQ   SEQUENCE   918 AA;  102495 MW;  FE7625FF3E3613EF CRC64;

  Query Match             16.4%;  Score 365.5;  DB 13;  Length 918;
  Best Local Similarity   30.1%;  Pred. No. 2.3e-23;
  Matches  102;  Conservative   44;  Mismatches  136;  Indels   57;  Gaps   14;

Qy      43 ISPQDPTLLIGSSLLATCSVHG---DPPGATAEGLYWTLNGRRLPPELSRVLNASTLALA 99
           | |: | | :||:  | | ::    |      |  : | :  : :| |  | :| :  ::
Db      34 IIPESPVLALGSNFTALCILNESCLDFGNIYASQIIWKMKNKVIPKEQYREINRTVSSVT 93

Qy     100 LANLNGSRQRSGDNLVCHA-RDGSI---LAGSCLYVGLPPEKPVNISC---------WSK 146
             : :         | |:   || |   : |  : |||||||| |:||        |
Db      94 FNDTSS----LASPLTCNVLADGQIEQNIYGISVTVGLPPEKPKNLSCIVYLSPKVEWYM 149

Qy     147 NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTP 206
           |     | | || |  ||| | : |||        :   ||     :|| |  |:  |
Db     150 N-----CTWNPGRH--TFLDTRFRLKYMWPRETFPDCIPEYVN---NSCTI-SDVQFFVN 198

Qy     207 YEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDF 266
            |:|||| | || | || |  | :::|   || :: |:  | |   | : | :   :
Db     199 LEVWVEAANALGKAESDHLVFDPIEIVKPPPPRNLSVNS-GILPTVLKLSWEN--QISTV 255

Qy     267 LFQAKYQIRYRVEDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKK 323
           : : |: ||||:    :|  |   |  | :||  : ||:| | |   :||
Db     256 VMELKFNIRYRISSDTNWMEVPPEDTASPRTSFSIQGLRPYTEYVFSIRC-----MKEDG 310

Qy     324 AGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGP 362
           | ||:||      |                :|| ||
Db     311 VGFWSDWSEEQIGVTTED--------------KPSKGP 334


RESULT 5
O57519
ID   O57519      PRELIMINARY;      PRT;   881 AA.
AC   O57519;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Gp130p1.
GN   XGP130.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chen J., Grace A., Chien K.R.;
RT   "Partial characterization of putative Xenopus gp130.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF041845; AAC03531.1; -.
DR   HSSP; P40189; 1BQU.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003529; Hemtopoptn_L_F2.
DR   Pfam; PF00041; fn3; 4.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
SQ   SEQUENCE   881 AA;  99003 MW;  7DE7942D211138A0 CRC64;

  Query Match             15.9%;  Score 354;  DB 13;  Length 881;
  Best Local Similarity   30.2%;  Pred. No. 2.2e-22;
  Matches   98;  Conservative   41;  Mismatches  125;  Indels   60;  Gaps   11;

Qy      62 VHGDPPGAT------------AEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQR 109
           |||: |                |  :|| : | ::|     :|| :| ::   ||
Db      37 VHGERPFTAYCVINQTCLREDASRIYWLVKGVKVPETQYEILNQTTSSVTFENLTTLNSP 96

Qy     110 SGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNY 169
             |::     : | |    :||||:|| |::|    |  :||| | ||    | | |||
Db      97 LTCNVMASGHVANTLYGIFFTLGLPPDKPTNLTCIVYNQDNLTCTWDPGR--PTNLPTNY 154

Qy     170 SLKYKLRW--------YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSAR 221
           :| :  ||         | :|:|         : | |     :      |||| ||  :
Db     155 TLSH--RWAHFGANYCRGANNSC---------TIHSP-GFQFYIDTTFQVEATNELGIQK 202

Qy     222 SDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDS 281
           |: ||:| :::|  :||    :     | : | : | :|       |  || ||||   :
Db     203 SETLTIDPVNIVKPNPPQLSELISSLELPNALKIEWKNPIT---NAFNLKYNIRYRPVKT 259

Qy     282 VDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAST 338
           ||::|   |  |:: |  |  | | ||| | :||          | ||:||    |
Db     260 QDWEMVPEEDTASHRDSFTLQDLLPNTVYEVSIRC-----IHKDGHGFWSDWSELKKQVT 314

Qy     339 PRSERPGPGGGACEPRGGEPSSGP 362
           |  | |              || ||
Db     315 P--EAP------------PSRGP 323


RESULT 6
Q8TD78
ID   Q8TD78      PRELIMINARY;      PRT;   268 AA.
AC   Q8TD78;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Prolactin receptor delta 7/11.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BREAST TUMOR;
RA   Trott J.F., Hovey R.C., Koduri S., Vonderhaar B.K.;
RT   "Expression of multiple human prolactin receptor variants in breast
```

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  Best Local Similarity   99.0%;  Pred. No. 1.2e-185;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           |||||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 2
Q9UHH5
ID   Q9UHH5      PRELIMINARY;      PRT;   422 AA.
AC   Q9UHH5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Class I cytokine receptor.
GN   ZCYTOR5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lok S., Presnell S.R., Jelmberg A.C., Gilbert T., Whitmore T.E.,
RA   Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF178684; AAD54385.1; -.
DR   HSSP; P16471; 1BP3.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   Pfam; PF00041; fn3; 2.
DR   SMART; SM00060; FN3; 1.
KW   Receptor.
SQ   SEQUENCE   422 AA;  46315 MW;  0D2C5F7A01B942EE CRC64;

  Query Match             98.6%;  Score 2198.5;  DB 4;  Length 422;
  Best Local Similarity   98.8%;  Pred. No. 2.7e-185;
  Matches  405;  Conservative    2;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPE 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           |||||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 3
Q9JM58
ID   Q9JM58      PRELIMINARY;      PRT;   425 AA.
AC   Q9JM58;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Cytokine receptor like molecule 3 precursor.
GN   CRLF1 OR CRLM3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.;
RT   "cytokine receptor like molecule 3.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB040038; BAA92777.1; -.
DR   HSSP; P16471; 1BP3.
DR   MGD; MGI:1340030; Crlf1.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   Pfam; PF00041; fn3; 2.
DR   SMART; SM00060; FN3; 1.
KW   Receptor; Signal.
FT   SIGNAL        1     34       POTENTIAL.
SQ   SEQUENCE   425 AA;  46662 MW;  910535C629CA7056 CRC64;

  Query Match             93.9%;  Score 2095;  DB 11;  Length 425;
  Best Local Similarity   93.9%;  Pred. No. 3.5e-176;
  Matches  388;  Conservative    6;  Mismatches   13;  Indels    6;  Gaps    3;

Qy       1 MPAGRRGPAAQSARRPP-PLLPLL--LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLL 57
           ||||| || |||||||| ||  |   ||||||| || ||||||||||||||||||||||
Db       1 MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ 60

Qy      58 ATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCH 117
           ||||:||| |||||||||||||||| ||||:|| |||||||||||||:||||||||||||
Db      61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH 120

Qy     118 ARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 177
           |||||||||||||||||| |||||:|||||||||||||||||||||||||||||||||||
Db     121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180

Qy     178 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDP 237
           ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db     181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP 240

Qy     238 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 300

Qy     298 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGE 357
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 13, 2003, 11:46:42 ; Search time 35.424 Seconds
(without alignments)
2384.805 Million cell updates/sec

Title: US-09-521-335-12
Perfect score: 2230
Sequence: 1 MPAGRRGPAAQSARRPPPLL.....WRAWMQKSHKTRNQVLPDKL 410

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2202.5	98.8	422	4	O75462	O75462 homo sapien
2	2198.5	98.6	422	4	Q9UHH5	Q9uhh5 homo sapien
3	2095	93.9	425	11	Q9JM58	Q9jm58 mus musculu
4	365.5	16.4	918	13	Q9W6U9	Q9w6u9 gallus gall
5	354	15.9	881	13	O57519	O57519 xenopus lae
6	333	14.9	268	4	Q8TD78	Q8td78 homo sapien
7	332	14.9	288	4	Q96P36	Q96p36 homo sapien
8	332	14.9	349	4	Q9UHJ5	Q9uhj5 homo sapien
9	332	14.9	376	4	Q96P35	Q96p35 homo sapien
10	325.5	14.6	206	4	Q16354	Q16354 homo sapien
11	317	14.2	622	6	Q9N0J7	Q9n0j7 callithrix
12	309.5	13.9	608	11	Q99JZ1	Q99jz1 mus musculu
13	294	13.2	611	13	Q9PTH9	Q9pth9 xenopus lae
14	292.5	13.1	611	13	Q9IBF6	Q9ibf6 xenopus lae
15	292.5	13.1	611	13	Q9PTI0	Q9pti0 xenopus lae
16	290	13.0	626	13	Q90WG7	Q90wg7 cynops pyrr
17	270.5	12.1	227	6	Q9GLW3	Q9glw3 ursus marit
18	270.5	12.1	346	13	O93404	O93404 oreochromis
19	270.5	12.1	625	6	Q9XS92	Q9xs92 trichosurus
20	270	12.1	636	13	Q90ZI6	Q90zi6 paralichthy
21	261.5	11.7	538	13	Q9DFU0	Q9dfu0 sparus aura
22	261	11.7	638	13	Q9DE08	Q9de08 oncorhynchu
23	246	11.0	861	6	Q9BEG2	Q9beg2 bos taurus
24	243.5	10.9	197	4	Q8TD76	Q8td76 homo sapien
25	243.5	10.9	1147	13	Q9DDK1	Q9ddk1 meleagris g
26	242.5	10.9	217	4	Q8TD75	Q8td75 homo sapien
27	242.5	10.9	1148	13	Q9IBA7	Q9iba7 gallus gall
28	240	10.8	600	13	Q9PTP0	Q9ptp0 carassius a
29	238.5	10.7	848	6	Q8WN24	Q8wn24 sus scrofa
30	237	10.6	372	11	O88507	O88507 mus musculu
31	237	10.6	1146	13	Q9I8V6	Q9i8v6 gallus gall
32	236	10.6	604	13	Q8QG54	Q8qg54 cyprinus ca
33	235.5	10.6	217	6	O46386	O46386 mustela vis
34	233.5	10.5	509	4	Q8WYJ0	Q8wyj0 homo sapien
35	231.5	10.4	198	6	O18985	O18985 cervus elap
36	211.5	9.5	422	4	Q16542	Q16542 homo sapien
37	208.5	9.3	432	11	Q64385	Q64385 mus musculu
38	208	9.3	431	11	Q99MF4	Q99mf4 rattus norv
39	200.5	9.0	1083	13	Q8QFQ7	Q8qfq7 gallus gall
40	199.5	8.9	432	11	P70225	P70225 mus musculu
41	195.5	8.8	1162	11	Q9QWG3	Q9qwg3 mus musculu
42	193.5	8.7	848	6	Q9MZS2	Q9mzs2 sus scrofa
43	193.5	8.7	1165	6	O02671	O02671 sus scrofa
44	192.5	8.6	710	13	O57520	O57520 xenopus lae
45	184	8.3	895	11	Q62960	Q62960 rattus norv

ALIGNMENTS

RESULT 1
O75462
ID O75462 PRELIMINARY; PRT; 422 AA.
AC O75462;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytokine-like factor-1 precursor.
GN CLF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elson G.C.A., Graber P., Losberger P., Herren S., Gretener D.,
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.F.;
RT "CLF-1, a Novel Soluble Protein Shares Homology With Members of the
RT Cytokine Type-I Receptor Family.";
RL J. Immunol. 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Magrangeas F., Jacques Y., Minvielle S.;
RT "Cloning and expression of a novel soluble protein containing
RT hematopoietic cytokine receptor domains.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF059293; AAC28335.1; -.
DR EMBL; AF073515; AAD39681.1; -.
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
KW Receptor; Signal.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.
SQ SEQUENCE 422 AA; 46301 MW; AD9DEFCB01B84228 CRC64;

Query Match 98.8%; Score 2202.5; DB 4; Length 422;

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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M31661; AAA60174.1; -.
DR   EMBL; AF091870; AAD32032.1; -.
DR   EMBL; AF091863; AAD32032.1; JOINED.
DR   EMBL; AF091864; AAD32032.1; JOINED.
DR   EMBL; AF091865; AAD32032.1; JOINED.
DR   EMBL; AF091866; AAD32032.1; JOINED.
DR   EMBL; AF091867; AAD32032.1; JOINED.
DR   EMBL; AF091868; AAD32032.1; JOINED.
DR   EMBL; AF091869; AAD32032.1; JOINED.
DR   EMBL; AF349939; AAK32703.1; -.
DR   PIR; A40144; A40144.
DR   PDB; 1BP3; 23-SEP-98.
DR   Genew; HGNC:9446; PRLR.
DR   MIM; 176761; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003528; Hemtopoptn_L_F1.
DR   Pfam; PF00041; fn3; 3.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW   Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW   Alternative splicing; 3D-structure.
FT   SIGNAL       1     24
FT   CHAIN       25    622       PROLACTIN RECEPTOR.
FT   DOMAIN      25    234       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   235    258       POTENTIAL.
FT   DOMAIN     259    622       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      25    122       FIBRONECTIN TYPE-III 1.
FT   DOMAIN     123    227       FIBRONECTIN TYPE-III 2.
FT   DISULFID    36     46       BY SIMILARITY.
FT   DISULFID    75     86       BY SIMILARITY.
FT   CARBOHYD    59     59       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   104    104       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   233    233       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    24    124       MISSING (IN ISOFORM 2).
SQ   SEQUENCE   622 AA;  69505 MW;  DB7FD0328608C787 CRC64;

  Query Match             14.9%;  Score 332;  DB 1;  Length 622;
  Best Local Similarity   37.1%;  Pred. No. 1.2e-18;
  Matches   83;  Conservative   28;  Mismatches   95;  Indels   18;  Gaps    8;

Qy     123 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 181
           :   :||  | |||  ||    | | | :  || | ||  |   | |||||  |
Db      15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72

Qy     182 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           : | :| | ||:|||  |   :::  | : | |||::||: || | :|:  :|  ||| :
Db      73 HECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLE 132

Qy     241 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 295
           : |  |   ||:    |:  ||| | |     |   |:|| : | : :|: :     ||
Db     133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTE 190

Qy     296 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 339
           ::  | ||  | ||||| |         | || ||  |    |
Db     191 FKILSLHPGQKYLVQVRCKP-------DHGYWSAWSPATFIQIP 227


RESULT 2
IL6B_HUMAN
ID   IL6B_HUMAN     STANDARD;      PRT;   918 AA.
AC   P40189; Q9UQ41;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE   6 signal transducer) (Membrane glycoprotein 130) (GP130) (Oncostatin M
DE   receptor) (CDw130) (CD130 antigen).
GN   IL6ST.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Myeloma, and Placenta;
RX   MEDLINE=91084844; PubMed=2261637;
RA   Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
RT   "Molecular cloning and expression of an IL-6 signal transducer,
RT   gp130.";
RL   Cell 63:1149-1157(1990).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Synovium;
RX   MEDLINE=20341529; PubMed=10880057;
RA   Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
RA   Murakami M., Nakao K.;
RT   "Cloning of novel soluble gp130 and detection of its neutralizing
RT   autoantibodies in rheumatoid arthritis.";
RL   J. Clin. Invest. 106:137-144(2000).
RN   [3]
RP   PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX   MEDLINE=21269388; PubMed=11098061;
RA   Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
RT   "Determination of the disulfide structure and N-glycosylation sites of
RT   the extracellular domain of the human signal transducer gp130.";
RL   J. Biol. Chem. 276:8244-8253(2001).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
RX   MEDLINE=98169383; PubMed=9501088;
RA   Bravo J., Staunton D., Heath J.K., Jones E.Y.;
RT   "Crystal structure of a cytokine-binding region of gp130.";
RL   EMBO J. 17:1665-1674(1998).
CC   -!- FUNCTION: Signal-transducing molecule. The receptor systems for
CC       IL-6, LIF, OSM, CNTF, IL-11 AND CT-1 can utilize gp130 for
CC       initiating signal transmission. Binds to IL-6/IL-6-R (alpha chain)
CC       complex, resulting in the formation of high-affinity IL-6 binding
CC       sites, and transduces the signal. Does not bind IL-6. May have a
CC       role in embryonic development (By similarity).
CC   -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC       Secreted (isoform 2).
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/gp130-
CC       RAPS; are produced by alternative splicing.
CC   -!- TISSUE SPECIFICITY: Found in all the tissues and cell lines
CC       examined. Expression not restricted to IL-6 responsive cells.
CC   -!- DISEASE: Isoform 2 is an autoantigen found in rheumatoid
CC       arthritis (RA) but it is not specific to patients with RA.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD130 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd130.htm".
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M57230; AAA59155.1; -.
DR   EMBL; AB015706; BAA78112.1; -.
DR   PIR; A36337; A36337.
DR   PDB; 1BQU; 26-AUG-98.
DR   Genew; HGNC:6021; IL6ST.
DR   MIM; 600694; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_repeat.
DR   InterPro; IPR003529; Hemtopoptn_L_F2.
DR   Pfam; PF00041; fn3; 3.
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 13, 2003, 11:41:52 ; Search time 11.808 Seconds
(without alignments)
1440.150 Million cell updates/sec

Title: US-09-521-335-12
Perfect score: 2230
Sequence: 1 MPAGRRGPAAQSARRPPPLL.....WRAWMQKSHKTRNQVLPDKL 410

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	332	14.9	622	1	PRLR_HUMAN	P16471 homo sapien
2	323	14.5	918	1	IL6B_HUMAN	P40189 homo sapien
3	317.5	14.2	917	1	IL6B_MOUSE	Q00560 mus musculu
4	316	14.2	830	1	PRLR_COLLI	Q90374 columba liv
5	314.5	14.1	918	1	IL6B_RAT	P40190 rattus norv
6	313	14.0	610	1	PRLR_RAT	P05710 rattus norv
7	309.5	13.9	581	1	PRLR_SHEEP	O46561 ovis aries
8	309.5	13.9	608	1	PRLR_MOUSE	Q08501 mus musculu
9	308	13.8	831	1	PRLR_CHICK	Q04594 gallus gall
10	307	13.8	831	1	PRLR_MELGA	Q91094 meleagris g
11	306.5	13.7	581	1	PRLR_BOVIN	Q28172 bos taurus
12	304	13.6	581	1	PRLR_CEREL	Q28235 cervus elap
13	300.5	13.5	616	1	PRLR_RABIT	P14787 oryctolagus
14	263.5	11.8	630	1	PRLR_ORENI	Q91513 oreochromis
15	256	11.5	837	1	GCSR_MOUSE	P40223 mus musculu
16	246	11.0	372	1	CNTR_RAT	Q08406 rattus norv
17	243	10.9	836	1	GCSR_HUMAN	Q99062 homo sapien
18	233.5	10.5	372	1	CNTR_HUMAN	P26992 homo sapien
19	223	10.0	467	1	IL6A_PIG	O18796 sus scrofa
20	213	9.6	862	1	I12S_HUMAN	Q99665 homo sapien
21	211.5	9.5	362	1	CNTR_CHICK	P51641 gallus gall
22	205.5	9.2	874	1	I12S_MOUSE	P97378 mus musculu
23	201.5	9.0	460	1	IL6A_MOUSE	P22272 mus musculu
24	201	9.0	468	1	IL6A_HUMAN	P08887 homo sapien
25	200	9.0	1097	1	LIFR_HUMAN	P42702 homo sapien
26	198.5	8.9	462	1	IL6A_RAT	P22273 rattus norv
27	194.5	8.7	1162	1	LEPR_MOUSE	P48356 mus musculu
28	194	8.7	625	1	TPOR_MOUSE	Q08351 mus musculu
29	190.5	8.5	1162	1	LEPR_RAT	Q62959 rattus norv
30	187	8.4	1092	1	LIFR_MOUSE	P42703 mus musculu
31	186.5	8.4	635	1	TPOR_HUMAN	P40238 homo sapien
32	178	8.0	1165	1	LEPR_HUMAN	P48357 homo sapien
33	169.5	7.6	427	1	I131_HUMAN	P78552 homo sapien
34	165.5	7.4	638	1	GHR_RABIT	P19941 oryctolagus
35	161.5	7.2	508	1	EPOR_HUMAN	P19235 homo sapien
36	160	7.2	888	1	UFO_MOUSE	Q00993 mus musculu
37	158.5	7.1	638	1	GHR_PIG	P19756 sus scrofa
38	158	7.1	507	1	EPOR_RAT	Q07303 rattus norv
39	156	7.0	507	1	EPOR_MOUSE	P14753 mus musculu
40	153	6.9	638	1	GHR_HUMAN	P10912 homo sapien
41	152	6.8	424	1	I131_MOUSE	O09030 mus musculu
42	151	6.8	1040	1	AXO1_RAT	P22063 rattus norv
43	151	6.8	2012	1	DSCA_HUMAN	O60469 homo sapien
44	150.5	6.7	897	1	CYRB_HUMAN	P32927 homo sapien
45	148.5	6.7	1036	1	AXO1_CHICK	P28685 gallus gall

ALIGNMENTS

RESULT 1
PRLR_HUMAN
ID PRLR_HUMAN STANDARD; PRT; 622 AA.
AC P16471; Q9BX87;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90114212; PubMed=2558309;
RA Boutin J.-M., Edery M., Shirota M., Jolicoeur C., Lesueur L.,
RA Ali S., Gould D., Djiane J., Kelly P.A.;
RT "Identification of a cDNA encoding a long form of prolactin receptor
RT in human hepatoma and breast cancer cells.";
RL Mol. Endocrinol. 3:1455-1461(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99182102; PubMed=10084611;
RA Hu Z.-Z., Zhuang L., Meng J., Leondires M., Dufau M.L.;
RT "The human prolactin receptor gene structure and alternative promoter
RT utilization: the generic promoter hPIII and a novel human promoter
RT hP(N).";
RL J. Clin. Endocrinol. Metab. 84:1153-1156(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Breast carcinoma;
RA Kline J.B., Clevenger C.V.;
RT "Characterization of a novel and functional human prolactin receptor
RT isoform (delta-S1 PRLr) containing only one extracellular
RT fibronectin-like domain.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.
RX MEDLINE=95075462; PubMed=7984244;
RA Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;
RT "The X-ray structure of a growth hormone-prolactin receptor complex.";
RL Nature 372:478-481(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Delta-S1;
CC are produced by alternative splicing.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC ---

```
Qy    296 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 339
          ::  | ||  | ||||| |         | || ||  |    |
Db    191 FKILSLHPGQKYLVQVRCKP-------DHGYWSAWSPATFIQIP 227


RESULT 2
A59405
prolactin receptor short form S1a precursor, breast cancer cells T-47D - human
C;Species: Homo sapiens
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002
C;Accession: A59405; A49400
R;Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A;Title: Isolation and characterization of two novel forms of the human prolactin recept
A;Reference number: A59405; MUID:21538812; PMID:11518703
A;Accession: A59405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <HU1>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
R;[illegible] Z.Z.
[illegible]itted to GenBank, December, 1999
A;Reference number: A49400
A;Accession: A49400
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <HU2>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
C;Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor
eta-casein gene promoter activation, with S1a less effective than S1b. However, their li
ted COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe
C;Genetics:
A;Gene: GDB:PRLR
A;Cross-references: GDB:120315; OMIM:176761
A;Map position: 5p13.3-5p13.1
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-376/Product: prolactin receptor, short form S1a #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             14.9%;  Score 332;  DB 2;  Length 376;
  Best Local Similarity   37.1%;  Pred. No. 2.1e-18;
  Matches   83;  Conservative   28;  Mismatches   95;  Indels   18;  Gaps    8;

Qy    123 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 181
          :   :||  | ||| ||    | | | :  || | ||  |   | |||||
Db     15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72

Qy    182 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
          : | :| | ||:|||  |   :::  | : | |||::||: || | :|:  :|  ||| :
Db     73 HECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLE 132

Qy    241 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 295
          : |  |   ||:    |:  ||| | |     |   |:|| : | : :|: :     ||
Db    133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTE 190

Qy    296 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 339
          ::  | ||  | ||||| |         | || ||  |    |
Db    191 FKILSLHPGQKYLVQVRCKP-------DHGYWSAWSPATFIQIP 227


RESULT 3
A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 01-Dec-2000
C;Accession: A40144; A57018
R;Boutin, J.M.; Edery, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D.;
Mol. Endocrinol. 3, 1455-1461, 1989
A;Title: Identification of a cDNA encoding a long form of prolactin receptor in human he
A;Reference number: A40144; MUID:90114212; PMID:2558309
A;Accession: A40144
A;Molecule type: mRNA
A;Residues: 1-622 <BOU>
A;Cross-references: GB:M31661; NID:g190361; PIDN:AAA60174.1; PID:g190362
R;Fuh, G.; Wells, J.A.
J. Biol. Chem. 270, 13133-13137, 1995
A;Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li
A;Reference number: A57018; MUID:95286597; PMID:7768908
A;Accession: A57018
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 25-228,'AW' <RES>
A;Cross-references: GB:S78505; NID:g999114; PIDN:AAB34470.1; PID:g999115
C;Genetics:
A;Gene: GDB:PRLR
A;Cross-references: GDB:120315; OMIM:176761
A;Map position: 5p13.3-5p13.1
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-622/Product: prolactin receptor, long form #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             14.9%;  Score 332;  DB 2;  Length 622;
  Best Local Similarity   37.1%;  Pred. No. 3.9e-18;
  Matches   83;  Conservative   28;  Mismatches   95;  Indels   18;  Gaps    8;

Qy    123 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 181
          :   :||  | ||| ||    | | | :  || | ||  |   | |||||
Db     15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72

Qy    182 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
          : | :| | ||:|||  |   :::  | : | |||::||: || | :|:  :|  ||| :
Db     73 HECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLE 132

Qy    241 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 295
          : |  |   ||:    |:  ||| | |     |   |:|| : | : :|: :     ||
Db    133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTE 190

Qy    296 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 339
          ::  | ||  | ||||| |         | || ||  |    |
Db    191 FKILSLHPGQKYLVQVRCKP-------DHGYWSAWSPATFIQIP 227


RESULT 4
A36337
membrane glycoprotein gp130 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
C;Accession: A36337
R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A;Reference number: A36337; MUID:91084844; PMID:2261637
A;Accession: A36337
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-918 <HIB>
A;Cross-references: GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354
C;Genetics:
A;Gene: GDB:IL6ST; GP130
A;Cross-references: GDB:126725; OMIM:600694
A;Map position: 5q11-5q11
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology <CRS>

  Query Match             14.5%;  Score 323;  DB 2;  Length 918;
  Best Local Similarity   28.2%;  Pred. No. 3.2e-17;
  Matches   87;  Conservative   52;  Mismatches  151;  Indels   18;  Gaps    8;

Qy     43 ISPQDPTLLIGSSLLATCSVHG---DPPGATAEGLYWTLNGRRLPPELSRVLNASTLALA 99
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 13, 2003, 11:48:13 ; Search time 18.368 Seconds
(without alignments)
2145.858 Million cell updates/sec

Title: US-09-521-335-12
Perfect score: 2230
Sequence: 1 MPAGRRGPAAQSARRPPPLL.....WRAWMQKSHKTRNQVLPDKL 410

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	332	14.9	288	2	B59405	prolactin receptor
2	332	14.9	376	2	A59405	prolactin receptor
3	332	14.9	622	2	A40144	prolactin receptor
4	323	14.5	918	2	A36337	membrane glycoprot
5	317.5	14.2	917	2	I49699	glycoprotein 130 -
6	316	14.2	830	2	I50455	prolactin receptor
7	314.5	14.1	918	2	A44257	interleukin-6 sign
8	313	14.0	310	2	A29884	prolactin receptor
9	313	14.0	412	2	A41070	prolactin receptor
10	313	14.0	610	2	A34631	lactogen receptor
11	313	14.0	610	2	A36116	prolactin receptor
12	309.5	13.9	292	2	I77525	prolactin receptor
13	309.5	13.9	303	2	I77524	prolactin receptor
14	309.5	13.9	608	2	I53269	prolactin receptor
15	308	13.8	831	2	JQ1655	prolactin receptor
16	306.5	13.7	581	2	I45971	prolactin receptor
17	300.5	13.5	616	2	A30304	prolactin receptor
18	263.5	11.8	630	2	I51086	prolactin receptor
19	256	11.5	837	2	A34898	granulocyte colony
20	246	11.0	372	2	I58141	ciliary neurotroph
21	243	10.9	771	2	B38252	granulocyte colony
22	243	10.9	783	2	JH0329	granulocyte colony
23	243	10.9	863	2	C38252	granulocyte colony
24	235.5	10.6	372	1	UHHUCN	ciliary neurotroph
25	211.5	9.5	362	2	S60614	growth promoting a
26	211.5	9.5	422	2	I37891	interleukin-11 rec
27	208.5	9.3	432	2	I48343	interleukin-11 rec
28	201.5	9.0	460	2	JL0145	interleukin-6 rece
29	201	9.0	468	1	A41242	interleukin-6 rece
30	200	9.0	1097	2	S17308	leukemia inhibitor
31	199	8.9	156	2	A32868	prolactin receptor
32	194.5	8.7	805	2	S68441	leptin receptor, s
33	194.5	8.7	892	2	S68439	leptin receptor, s
34	194.5	8.7	894	2	S68437	leptin receptor, s
35	194.5	8.7	900	2	S68440	leptin receptor, s
36	194.5	8.7	1162	2	S68438	leptin receptor, s
37	194	8.7	625	2	S35317	hematopoietic grow
38	192.5	8.6	440	2	JL0144	interleukin-6 rece
39	191	8.6	150	2	B34631	lactogen receptor
40	190.5	8.5	1162	2	PC4184	leptin receptor, O
41	190	8.5	626	2	S37622	proto-oncogene - m
42	187	8.4	1092	2	JX0312	differentiation-st
43	186.5	8.4	579	2	B45266	MPL-K protein prec
44	186.5	8.4	635	2	A45266	MPL-P protein prec
45	184	8.3	895	2	S74225	leptin receptor, i

ALIGNMENTS

RESULT 1
B59405
prolactin receptor short form S1b precursor, breast cancer cells T-47D - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002
C;Accession: B59405; B49400
R;Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A;Title: Isolation and characterization of two novel forms of the human prolactin recepto
A;Reference number: A59405; MUID:21538812; PMID:11518703
A;Accession: B59405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-288 <HU1>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
R;Hu, Z.Z.
submitted to GenBank, December, 1999
A;Reference number: A49400
A;Accession: B49400
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-288 <HU2>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
C;Comment: This is one of the short forms (S1a and S1b) of the human proactin receptor ge
ta-casein gene promoter activation, with S1b more effective than S1a. However, their liga
C;Genetics:
A;Gene: GDB:PRLR
A;Cross-references: GDB:120315; OMIM:176761
A;Map position: 5p13.3-5p13.1
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-288/Product: prolactin receptor, short form S1b #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.9%; Score 332; DB 2; Length 288;
Best Local Similarity 37.1%; Pred. No. 1.5e-18;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

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Qy    123 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 181
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Db     15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72

Qy    182 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
          : | :| | ||:||| |   :::  | : | |||::||: || | :|:  :|  ||| :
Db     73 HECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLE 132

Qy    241 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 295
          : |  |   ||:    |:  ||| | |     |   |:|| : | : :|: :     ||
Db    133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTE 190
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; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-862-32

Query Match 98.8%; Score 2202.5; DB 10; Length 422;
Best Local Similarity 99.0%; Pred. No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

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Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
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Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
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Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
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Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410
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RESULT 12
[redacted]9-945-587-32
[redacted]quence 32, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678

; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
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; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-32

Query Match 98.8%; Score 2202.5; DB 10; Length 422;
Best Local Similarity 99.0%; Pred. No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

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Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
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Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
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Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
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Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
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Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
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Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
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Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410
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RESULT 11
US-09-944-862-32
; Sequence 32, Application US/09944862
; Patent No. US20020115145A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,862
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042

; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
; [redacted]9-944-449-32

Query Match 98.8%; Score 2202.5; DB 10; Length 422;
Best Local Similarity 99.0%; Pred. No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

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Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
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Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
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Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
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Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
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Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
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Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
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Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
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Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410
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RESULT 10
US-09-944-457-32
; Sequence 32, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
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; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
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; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
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; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841

; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
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; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; [redacted]MBER OF SEQ ID NOS: 120
; [redacted]Q ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-32

Query Match 98.8%; Score 2202.5; DB 10; Length 422;
Best Local Similarity 99.0%; Pred. No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

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Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           |||||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410
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RESULT 9
US-09-944-449-32
; Sequence 32, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,449
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: Decemberl, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565

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RESULT 6
US-09-944-907-32
; Sequence 32, Application US/09944907
; Publication No. US20020198147A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,907
;  CURRENT FILING DATE:  2001-08-31
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-944-907-32

  Query Match             98.8%;  Score 2202.5;  DB 9;  Length 422;
  Best Local Similarity   99.0%;  Pred. No. 3.8e-157;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           |||||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 7
US-09-944-929-32
; Sequence 32, Application US/09944929
; Publication No. US20020197612A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,929
;  CURRENT FILING DATE:  2001-08-31
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-944-929-32

  Query Match             98.8%;  Score 2202.5;  DB 9;  Length 422;
  Best Local Similarity   99.0%;  Pred. No. 3.8e-157;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
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Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           |||||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 8
US-09-866-028-32
; Sequence 32, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
```

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Qy    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
          ||||||||||||||||||||||||||||||||||||||||||||||   :||
Db    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 5
US-09-944-944-32
; Sequence 32, Application US/09944944
; Patent No. US20020173463A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,944
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-944-944-32

  Query Match             98.8%;  Score 2202.5;  DB 9;  Length 422;
  Best Local Similarity   99.0%;  Pred. No. 3.8e-157;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy      1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
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Qy     61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
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Db     61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy    121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy    181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
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Db    181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy    241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
          ||||||||||||||||||||||||||||||||||||||||||||||   :||
Db    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410
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Db    241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
          |||||||||||||||||||||||||||||||||||||||||||   :||
Db    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 4
US-09-944-896-32
; Sequence 32, Application US/09944896
; Patent No. US20020168715A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,896
;  CURRENT FILING DATE:  2001-08-31
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
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;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020168715Alember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020168715Alember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-944-896-32

  Query Match             98.8%;  Score 2202.5;  DB 9;  Length 422;
  Best Local Similarity   99.0%;  Pred. No. 3.8e-157;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

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RESULT 3
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; Patent No. US20020165143A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,403
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069335
;  PRIOR FILING DATE: December 11, 1997
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;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
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;  PRIOR APPLICATION NUMBER: 60/069,694
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;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/069,873
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;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
;  PRIOR APPLICATION NUMBER: 09/216,021
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 09/218,517
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: September 15, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28409
;  PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/28301
;  PRIOR FILING DATE: December1, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: December 16, 1999
;  PRIOR APPLICATION NUMBER: PCT/US00/03565
;  PRIOR FILING DATE: February 11, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: February 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: March 2, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/08439
;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-944-403-32

  Query Match             98.8%;  Score 2202.5;  DB 9;  Length 422;
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  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

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Qy    121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
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Qy    181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,413
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
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; PRIOR FILING DATE: September 15, 1999
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; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-413-32

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  Best Local Similarity   99.0%;  Pred. No. 3.8e-157;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 199416

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2202.5	98.8	422	9	US-09-944-944-32	Sequence 32, Appl
6	2202.5	98.8	422	9	US-09-944-907-32	Sequence 32, Appl
7	2202.5	98.8	422	9	US-09-944-929-32	Sequence 32, Appl
8	2202.5	98.8	422	10	US-09-866-028-32	Sequence 32, Appl
9	2202.5	98.8	422	10	US-09-944-449-32	Sequence 32, Appl
10	2202.5	98.8	422	10	US-09-944-457-32	Sequence 32, Appl
11	2202.5	98.8	422	10	US-09-944-862-32	Sequence 32, Appl
12	2202.5	98.8	422	10	US-09-945-587-32	Sequence 32, Appl
13	2202.5	98.8	422	10	US-09-945-015-32	Sequence 32, Appl
14	2202.5	98.8	422	10	US-09-944-396-32	Sequence 32, Appl
15	2202.5	98.8	422	10	US-09-944-097-32	Sequence 32, Appl
16	2202.5	98.8	422	10	US-09-944-432-32	Sequence 32, Appl
17	2202.5	98.8	422	10	US-09-943-762-32	Sequence 32, Appl
18	2202.5	98.8	422	10	US-09-944-654-32	Sequence 32, Appl
19	2202.5	98.8	422	10	US-09-943-851A-32	Sequence 32, Appl
20	2198.5	98.6	422	10	US-09-880-578-2	Sequence 2, Appli
21	2197.5	98.5	425	10	US-09-880-578-4	Sequence 4, Appli
22	2188	98.1	421	10	US-09-037-657-44	Sequence 44, Appl
23	2120	95.1	434	9	US-10-074-901-4	Sequence 4, Appli
24	2114.5	94.8	413	10	US-09-037-657-13	Sequence 13, Appl
25	2095	93.9	425	10	US-09-037-657-15	Sequence 15, Appl
26	2088	93.6	425	10	US-09-880-578-6	Sequence 6, Appli
27	2037	91.3	392	10	US-09-880-578-18	Sequence 18, Appl
28	2027.5	90.9	405	9	US-10-074-901-2	Sequence 2, Appli
29	2021	90.6	389	10	US-09-880-578-22	Sequence 22, Appl
30	2020	90.6	389	10	US-09-880-578-28	Sequence 28, Appl
31	2020	90.6	389	10	US-09-880-578-29	Sequence 29, Appl
32	2019	90.5	389	10	US-09-880-578-30	Sequence 30, Appl
33	2018	90.5	389	10	US-09-880-578-24	Sequence 24, Appl
34	2018	90.5	389	10	US-09-880-578-25	Sequence 25, Appl
35	2018	90.5	389	10	US-09-880-578-27	Sequence 27, Appl
36	2017	90.4	389	10	US-09-880-578-26	Sequence 26, Appl
37	2016.5	90.4	388	10	US-09-880-578-17	Sequence 17, Appl
38	2016	90.4	389	10	US-09-880-578-31	Sequence 31, Appl
39	2000.5	89.7	385	10	US-09-880-578-20	Sequence 20, Appl
40	1963.5	88.0	385	10	US-09-880-578-19	Sequence 19, Appl
41	1812	81.3	350	10	US-09-037-657-25	Sequence 25, Appl
42	1687.5	75.7	544	9	US-10-056-984-3	Sequence 3, Appli
43	1645	73.8	303	10	US-09-880-578-23	Sequence 23, Appl
44	1641	73.6	303	10	US-09-880-578-21	Sequence 21, Appl
45	1463	65.6	278	10	US-09-037-657-19	Sequence 19, Appl

ALIGNMENTS

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RESULT 1
US-10-056-984-2
; Sequence 2, Application US/10056984
; Publication No. US20030045683A1
; GENERAL INFORMATION:
;  APPLICANT: Cosman, David J.
;  APPLICANT:  Mosley, Bruce
;  TITLE OF INVENTION: H14 DNA and Polypeptides
;  FILE REFERENCE: 03260.0085-00000
;  CURRENT APPLICATION NUMBER: US/10/056,984
;  CURRENT FILING DATE:  2002-01-25
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/392,746
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/070,885
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/00516
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 426
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-056-984-2

  Query Match             99.2%;  Score 2212;  DB 9;  Length 426;
  Best Local Similarity   96.2%;  Pred. No. 7.4e-158;
  Matches  410;  Conservative    0;  Mismatches    0;  Indels   16;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
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Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
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Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
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Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
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Qy    218 GSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 277
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Db    181 GSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 240

Qy    278 VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS 337
          ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db    241 VEDSVDWKVVDDVSNQTSCRIAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS 300

Qy    338 TPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK 397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK 360

Qy    398 SHKTRNQ----------------VLPDKL 410
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Db    361 SHKTRNQHRTRGSCPRADGARREVLPDKL 389


RESULT 14
US-09-071-224-24
; Sequence 24, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Presnell, Scott R.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Gilbert, Teresa
;    APPLICANT:  Foster, Donald C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Lehner, Joyce M.
;    TITLE OF INVENTION:  MAMMALIAN ZCYTOR5
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zymogenetics
;      STREET:  1201 Eastlake Ave East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,224
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-224-24

  Query Match             90.5%;  Score 2018;  DB 4;  Length 389;
  Best Local Similarity   95.6%;  Pred. No. 5.2e-188;
  Matches  372;  Conservative    1;  Mismatches    0;  Indels   16;  Gaps    1;

Qy     38 AHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA 97
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Db      1 AHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA 60

Qy     98 LALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP 157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP 120

Qy    158 GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL 217
          |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GSHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL 180

Qy    218 GSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 240

Qy    278 VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS 337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS 300

Qy    338 TPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK 397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK 360

Qy    398 SHKTRNQ----------------VLPDKL 410
          |||||||                ||||||
Db    361 SHKTRNQHRTRGSCPRADGARREVLPDKL 389


RESULT 15
US-09-071-224-25
; Sequence 25, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Presnell, Scott R.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Gilbert, Teresa
;    APPLICANT:  Foster, Donald C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Lehner, Joyce M.
;    TITLE OF INVENTION:  MAMMALIAN ZCYTOR5
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zymogenetics
;      STREET:  1201 Eastlake Ave East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,224
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
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; Sequence 29, Application US/09071224
; Patent No. 6271343
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Presnell, Scott R.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Gilbert, Teresa
;    APPLICANT:  Foster, Donald C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Lehner, Joyce M.
;    TITLE OF INVENTION:  MAMMALIAN ZCYTOR5
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zymogenetics
;      STREET:  1201 Eastlake Ave East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,224
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-224-29

  Query Match             90.6%;  Score 2020;  DB 4;  Length 389;
  Best Local Similarity   95.6%;  Pred. No. 3.3e-188;
  Matches  372;  Conservative    1;  Mismatches    0;  Indels   16;  Gaps    1;

Qy      38 AHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA 97
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Db       1 AHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA 60

Qy      98 LALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP 157
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Db      61 LALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP 120

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Db     121 GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL 180

Qy     218 GSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 277
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Db     181 GSARSDVLTLDILDIVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 240

Qy     278 VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS 337
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Db     241 VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS 300

Qy     338 TPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK 397
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Qy     398 SHKTRNQ----------------VLPDKL 410
           |||||||                ||||||
Db     361 SHKTRNQHRTRGSCPRADGARREVLPDKL 389


RESULT 13
US-09-071-224-30
; Sequence 30, Application US/09071224
; Patent No. 6271343
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Presnell, Scott R.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Gilbert, Teresa
;    APPLICANT:  Foster, Donald C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Lehner, Joyce M.
;    TITLE OF INVENTION:  MAMMALIAN ZCYTOR5
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zymogenetics
;      STREET:  1201 Eastlake Ave East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,224
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-224-30

  Query Match             90.5%;  Score 2019;  DB 4;  Length 389;
  Best Local Similarity   95.6%;  Pred. No. 4.2e-188;
  Matches  372;  Conservative    1;  Mismatches    0;  Indels   16;  Gaps    1;

Qy      38 AHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA 97
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA 60

Qy      98 LALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP 157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP 120

Qy     158 GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL 217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL 180
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;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,224
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-224-22

  Query Match             90.6%;  Score 2021;  DB 4;  Length 389;
  Best Local Similarity   95.9%;  Pred. No. 2.7e-188;
  Matches  373;  Conservative    0;  Mismatches    0;  Indels   16;  Gaps    1;

Qy      38 AHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA 97
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA 60

Qy      98 LALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP 157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP 120

Qy     158 GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL 217
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Db     121 GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL 180

Qy     218 GSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 240

Qy     278 VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS 337
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Db     241 VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS 300

Qy     338 TPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK 397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK 360

Qy     398 SHKTRNQ----------------VLPDKL 410
           |||||||                ||||||
Db     361 SHKTRNQHRTRGSCPRADGARREVLPDKL 389


RESULT 11
US-09-071-224-28
; Sequence 28, Application US/09071224
; Patent No. 6271343
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Presnell, Scott R.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Gilbert, Teresa
;    APPLICANT:  Foster, Donald C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Lehner, Joyce M.
;    TITLE OF INVENTION:  MAMMALIAN ZCYTOR5
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zymogenetics
;      STREET:  1201 Eastlake Ave East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,224
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  389 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-224-28

  Query Match             90.6%;  Score 2020;  DB 4;  Length 389;
  Best Local Similarity   95.6%;  Pred. No. 3.3e-188;
  Matches  372;  Conservative    1;  Mismatches    0;  Indels   16;  Gaps    1;

Qy      38 AHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA 97
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA 60

Qy      98 LALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP 157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP 120

Qy     158 GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL 217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL 180

Qy     218 GSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 277
           ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 240

Qy     278 VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS 337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS 300

Qy     338 TPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK 397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK 360

Qy     398 SHKTRNQ----------------VLPDKL 410
           |||||||                ||||||
Db     361 SHKTRNQHRTRGSCPRADGARREVLPDKL 389


RESULT 12
US-09-071-224-29
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Db    121 WTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEAT 180

Qy    215 NRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQI 274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 NRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQI 240

Qy    275 RYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPT 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 RYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPT 300

Qy    335 AASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAW 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAW 360

Qy    395 MQKSHKTRNQ----------------VLPDKL 410
          ||||||||||                ||||||
Db    361 MQKSHKTRNQHRTRGSCPRADGARREVLPDKL 392
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RESULT 8
US-09-012-072-2
; Sequence 2, Application US/09012072
; Patent No. 6060276
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6060276el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/012,072
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-012-072-2

Query Match 90.9%; Score 2027.5; DB 3; Length 405;
Best Local Similarity 95.6%; Pred. No. 6.6e-189;
Matches 370; Conservative 6; Mismatches 8; Indels 3; Gaps 1;

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Qy     24 LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRL 83
          ||||||| || |||||||||||||||||||||| ||||:||| ||||||||||||||||||
Db      7 LLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRL 66

Qy     84 PPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISC 143
          | ||||:|| |||||||||||||:||||||||||||||||||||||||||||| ||||
Db     67 PSELSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISC 126

Qy    144 WSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLAL 203
          ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 WSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLAL 186

Qy    204 FTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPAL 263
          |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db    187 FTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPAL 246

Qy    264 KDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKK 323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 KDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKK 306

Qy    324 AGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNL 383
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    307 AGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNL 366

Qy    384 SFRLYDQWRAWMQKSHKTRNQ---VLP 407
          |||||||||||||||||||||   :||
Db    367 SFRLYDQWRAWMQKSHKTRNQDEGILP 393
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RESULT 9
US-09-120-601-2
; Sequence 2, Application US/09120601
; Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-120-601-2

Query Match 90.9%; Score 2027.5; DB 4; Length 405;
Best Local Similarity 95.6%; Pred. No. 6.6e-189;
Matches 370; Conservative 6; Mismatches 8; Indels 3; Gaps 1;

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Qy     24 LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRL 83
          ||||||| || |||||||||||||||||||||| ||||:||| ||||||||||||||||||
Db      7 LLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRL 66

Qy     84 PPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISC 143
          | ||||:|| |||||||||||||:||||||||||||||||||||||||||||| ||||
Db     67 PSELSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISC 126

Qy    144 WSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLAL 203
          ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 WSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLAL 186

Qy    204 FTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPAL 263
          |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db    187 FTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPAL 246

Qy    264 KDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKK 323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 KDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKK 306

Qy    324 AGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNL 383
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    307 AGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNL 366

Qy    384 SFRLYDQWRAWMQKSHKTRNQ---VLP 407
          |||||||||||||||||||||   :||
Db    367 SFRLYDQWRAWMQKSHKTRNQDEGILP 393
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RESULT 10
US-09-071-224-22
; Sequence 22, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTOR5
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:

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US-09-071-224-6
; Sequence 6, Application US/09071224
; Patent No. 6271343
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Presnell, Scott R.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Gilbert, Teresa
;    APPLICANT:  Foster, Donald C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Lehner, Joyce M.
;    TITLE OF INVENTION:  MAMMALIAN ZCYTOR5
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zymogenetics
;      STREET:  1201 Eastlake Ave East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,224
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  425 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
;9-071-224-6

  Query Match             93.6%;  Score 2088;  DB 4;  Length 425;
  Best Local Similarity   93.5%;  Pred. No. 9.3e-195;
  Matches  386;  Conservative    7;  Mismatches   14;  Indels    6;  Gaps    2;

Qy       1 MPAGRRGPAAQSARRPPPLLPLL---LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLL 57
           ||||  ||||||||||  |  |   |||||| |: ||||||||||||||||||||
Db       1 MPAGGPGPAAQSARRPPRRLSSLWSPLLLCVLGVPQGGSGAHTAVISPQDPTLLIGSSLH 60

Qy      58 ATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCH 117
           ||||:||| |||||||||||||||||| ||||:|| |||||||||||||:||||||||
Db      61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH 120

Qy     118 ARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 177
           |||||||||||||||||| ||||||:|||||||||||||||||||||||||||||||||
Db     121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180

Qy     178 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDP 237
           |||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db     181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP 240

Qy     238 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR 300

Qy     298 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGE 357
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db     301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE 360

Qy     358 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           |||||||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 413


RESULT 7
US-09-071-224-18
; Sequence 18, Application US/09071224
; Patent No. 6271343
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Presnell, Scott R.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Gilbert, Teresa
;    APPLICANT:  Foster, Donald C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Lehner, Joyce M.
;    TITLE OF INVENTION:  MAMMALIAN ZCYTOR5
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zymogenetics
;      STREET:  1201 Eastlake Ave East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,224
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  392 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-071-224-18

  Query Match             91.3%;  Score 2037;  DB 4;  Length 392;
  Best Local Similarity   95.9%;  Pred. No. 7.5e-190;
  Matches  376;  Conservative    0;  Mismatches    0;  Indels   16;  Gaps    1;

Qy      35 GSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNAS 94
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNAS 60

Qy      95 TLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCR 154
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCR 120

Qy     155 WTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEAT 214
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Qy      1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy     61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy    121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy    181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILD--------- 231
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVGSHLPLPS 240

Qy    232 ------------VVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRV 278
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PATPGLSLLVRGKVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRV 300

Qy    279 EDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAST 338
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 EDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAST 360

Qy    339 PRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKS 398
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKS 420

Qy    399 HKTRNQ----------------VLPDKL 410
          ||||||                ||||||
Db    421 HKTRNQHRTRGSCPRADGARREVLPDKL 448
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RESULT 4
US-09-012-072-4
; Sequence 4, Application US/09012072
; Patent No. 6060276
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6060276el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/012,072
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 434
; TYPE: PRT
; ORGANISM: HUMAN
US-09-012-072-4

Query Match 95.1%; Score 2120; DB 3; Length 434;
Best Local Similarity 91.2%; Pred. No. 7.4e-198;
Matches 396; Conservative 0; Mismatches 0; Indels 38; Gaps 2;

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Qy     15 RPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGL 74
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 RPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGL 60

Qy     75 YWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLP 134
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 YWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLP 120

Qy    135 PEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 PEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 180

Qy    195 CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILD----------------------V 232
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Db    181 CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVGSHLPLPSPATPGLSLLVRGKV 240

Qy    233 VTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSN 292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSN 300

Qy    293 QTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACE 352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 QTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACE 360

Qy    353 PRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ-------- 404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQHRTRGSCP 420

Qy    405 --------VLPDKL 410
                  ||||||
Db    421 RADGARREVLPDKL 434
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RESULT 5
US-09-120-601-4
; Sequence 4, Application US/09120601
; Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 434
; TYPE: PRT
; ORGANISM: HUMAN
US-09-120-601-4

Query Match 95.1%; Score 2120; DB 4; Length 434;
Best Local Similarity 91.2%; Pred. No. 7.4e-198;
Matches 396; Conservative 0; Mismatches 0; Indels 38; Gaps 2;

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Qy     15 RPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGL 74
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Qy     75 YWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLP 134
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Db     61 YWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLP 120

Qy    135 PEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 194
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Qy    195 CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILD----------------------V 232
          |||||||||||||||||||||||||||||||||||||                      |
Db    181 CHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVGSHLPLPSPATPGLSLLVRGKV 240

Qy    233 VTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSN 292
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Db    241 VTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSN 300

Qy    293 QTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACE 352
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Db    301 QTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACE 360

Qy    353 PRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ-------- 404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQHRTRGSCP 420

Qy    405 --------VLPDKL 410
                  ||||||
Db    421 RADGARREVLPDKL 434
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RESULT 6

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  Query Match             98.6%;  Score 2198.5;  DB 4;  Length 422;
  Best Local Similarity   98.8%;  Pred. No. 1.6e-205;
  Matches  405;  Conservative    2;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
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Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
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Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPE 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
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Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
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Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 2
US-09-071-224-4
; Sequence 4, Application US/09071224
; Patent No. 6271343
;  GENERAL INFORMATION:
;    APPLICANT:  Lok, Si
;    APPLICANT:  Presnell, Scott R.
;    APPLICANT:  Jelmberg, Anna C.
;    APPLICANT:  Gilbert, Teresa
;    APPLICANT:  Foster, Donald C.
;    APPLICANT:  Adams, Robyn L.
;    APPLICANT:  Lehner, Joyce M.
;    TITLE OF INVENTION:  MAMMALIAN ZCYTOR5
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Zymogenetics
;      STREET:  1201 Eastlake Ave East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/071,224
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  96-22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6627
;      TELEFAX:  206-442-6678
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  425 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-09-071-224-4

  Query Match             98.5%;  Score 2197.5;  DB 4;  Length 425;
  Best Local Similarity   96.0%;  Pred. No. 2.1e-205;
  Matches  409;  Conservative    0;  Mismatches    0;  Indels   17;  Gaps    2;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
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Db       1 MPAGRRGPAAQSARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 59

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 119

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     120 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 179

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 239

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 299

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 359

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---------------- 404
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Db     360 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQHRTRGSCPRADGARRE 419

Qy     405 VLPDKL 410
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RESULT 3
US-09-120-601-6
; Sequence 6, Application US/09120601
; Patent No. 6207413
; GENERAL INFORMATION:
;  APPLICANT: Masiakowski, Piotr
;  TITLE OF INVENTION: No. 6207413el Orphan Receptors
;  FILE REFERENCE: REG 630
;  CURRENT APPLICATION NUMBER: US/09/120,601
;  CURRENT FILING DATE: 1998-07-22
;  EARLIER APPLICATION NUMBER: 09/012,072
;  EARLIER FILING DATE: 1998-01-22
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-120-601-6

  Query Match             98.3%;  Score 2191;  DB 4;  Length 448;
  Best Local Similarity   91.5%;  Pred. No. 9.6e-205;
  Matches  410;  Conservative    0;  Mismatches    0;  Indels   38;  Gaps    2;
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GenCore version 5.1.4_p5_4578

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Run on: March 13, 2003, 11:47:42 ; Search time 16.4 Seconds
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735.573 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2197.5	98.5	425	4	US-09-071-224-4	Sequence 4, Appli
3	2191	98.3	448	4	US-09-120-601-6	Sequence 6, Appli
4	2120	95.1	434	3	US-09-012-072-4	Sequence 4, Appli
5	2120	95.1	434	4	US-09-120-601-4	Sequence 4, Appli
6	2088	93.6	425	4	US-09-071-224-6	Sequence 6, Appli
7	2037	91.3	392	4	US-09-071-224-18	Sequence 18, Appl
8	2027.5	90.9	405	3	US-09-012-072-2	Sequence 2, Appli
9	2027.5	90.9	405	4	US-09-120-601-2	Sequence 2, Appli
10	2021	90.6	389	4	US-09-071-224-22	Sequence 22, Appl
11	2020	90.6	389	4	US-09-071-224-28	Sequence 28, Appl
12	2020	90.6	389	4	US-09-071-224-29	Sequence 29, Appl
13	2019	90.5	389	4	US-09-071-224-30	Sequence 30, Appl
14	2018	90.5	389	4	US-09-071-224-24	Sequence 24, Appl
15	2018	90.5	389	4	US-09-071-224-25	Sequence 25, Appl
16	2018	90.5	389	4	US-09-071-224-27	Sequence 27, Appl
17	2017	90.4	389	4	US-09-071-224-26	Sequence 26, Appl
18	2016.5	90.4	388	4	US-09-071-224-17	Sequence 17, Appl
19	2016	90.4	389	4	US-09-071-224-31	Sequence 31, Appl
20	2000.5	89.7	385	4	US-09-071-224-20	Sequence 20, Appl
21	1963.5	88.0	385	4	US-09-071-224-19	Sequence 19, Appl
22	1645	73.8	303	4	US-09-071-224-23	Sequence 23, Appl
23	1641	73.6	303	4	US-09-071-224-21	Sequence 21, Appl
24	332	14.9	349	3	US-08-806-597A-14	Sequence 14, Appl
25	332	14.9	349	3	US-08-970-428A-14	Sequence 14, Appl
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27	323	14.5	488	2	US-08-599-455B-5	Sequence 5, Appli
28	323	14.5	488	4	US-09-069-781B-5	Sequence 5, Appli
29	323	14.5	488	4	US-09-137-132-5	Sequence 5, Appli
30	323	14.5	488	4	US-08-864-564A-5	Sequence 5, Appli
31	323	14.5	488	4	US-09-094-410-5	Sequence 5, Appli
32	323	14.5	658	2	US-08-825-558-4	Sequence 4, Appli
33	323	14.5	658	4	US-09-312-611-4	Sequence 4, Appli
34	323	14.5	708	1	US-07-797-556-2	Sequence 2, Appli
35	323	14.5	708	1	US-08-308-881-2	Sequence 2, Appli
36	323	14.5	708	2	US-09-058-263-2	Sequence 2, Appli
37	323	14.5	708	2	US-09-059-099-2	Sequence 2, Appli
38	323	14.5	708	3	US-09-058-264-2	Sequence 2, Appli
39	323	14.5	708	5	PCT-US95-06530-2	Sequence 2, Appli
40	323	14.5	918	2	US-08-825-558-6	Sequence 6, Appli
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42	311.5	14.0	592	4	US-09-000-145-6	Sequence 6, Appli
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44	256	11.5	837	1	US-07-923-976-2	Sequence 2, Appli
45	243	10.9	771	1	US-07-923-976-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-071-224-2
; Sequence 2, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTOR5
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-071-224-2

GenCore version 5.1.4_p5_4578

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Run on: March 13, 2003, 11:41:12 ; Search time 43.296 Seconds
(without alignments)
1261.843 Million cell updates/sec

Title: US-09-521-335-12
Perfect score: 2230
Sequence: 1 MPAGRRGPAAQSARRPPPLL.....WRAWMQKSHKTRNQVLPDKL 410

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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4	2212	99.2	426	20	AAY28281	Amino acid sequenc
5	2202.5	98.8	422	20	AAY26339	Human U4 haematopo
6	2202.5	98.8	422	20	AAY06479	Human tumour-assoc
7	2202.5	98.8	422	20	AAY17825	Human PRO327 prote
8	2202.5	98.8	422	20	AAY05782	Human type 1 cytok
9	2202.5	98.8	422	21	AAY93686	Amino acid sequenc
10	2202.5	98.8	422	21	AAB01316	Human PRO327 polyp
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13	2200	98.7	457	23	ABB06125	Human NS protein s
14	2198.5	98.6	422	20	AAW70860	Human Zcytor5 prot
15	2197.5	98.5	425	20	AAW70861	Allelic varaint of
16	2191	98.3	448	21	AAY44840	Human orphan cytok
17	2188	98.1	421	22	AAE00826	Murine haemopoieti
18	2131.5	95.6	408	19	AAW59805	Amino acid sequenc
19	2131.5	95.6	408	20	AAY26338	Human U4 haematopo
20	2120	95.1	434	20	AAY15215	Amino acid sequenc
21	2114.5	94.8	413	19	AAW55011	Novel haemopoietin
22	2114.5	94.8	413	21	AAY93658	A murine hemopoiet
23	2114.5	94.8	413	22	AAE00820	Murine haemopoieti
24	2095	93.9	425	19	AAW55012	Novel haemopoietin
25	2095	93.9	425	21	AAY93659	A murine hemopoiet
26	2095	93.9	425	22	AAE00821	Murine haemopoieti
27	2091	93.8	425	19	AAW59804	Nucleotide sequenc
28	2091	93.8	425	20	AAY26337	Murine U4 haematop
29	2088	93.6	425	20	AAW70862	Rat Zcytor5 protei
30	2037	91.3	392	20	AAW70840	Human Zcytor5 vari
31	2028.5	91.0	416	20	AAY29780	Mouse DNAX soluble
32	2027.5	90.9	405	20	AAY15214	Amino acid sequenc
33	2027.5	90.9	405	21	AAY44839	Mouse orphan cytok
34	2021	90.6	389	20	AAW70844	Human Zcytor5 vari
35	2020	90.6	389	20	AAW70850	Human Zcytor5 vari
36	2020	90.6	389	20	AAW70851	Human Zcytor5 vari
37	2019	90.5	389	20	AAW70852	Human Zcytor5 vari
38	2018	90.5	389	20	AAW70846	Human Zcytor5 vari
39	2018	90.5	389	20	AAW70847	Human Zcytor5 vari
40	2018	90.5	389	20	AAW70849	Human Zcytor5 vari
41	2017	90.4	389	20	AAW70848	Human Zcytor5 vari
42	2016.5	90.4	388	20	AAW70839	Human Zcytor5 vari
43	2016	90.4	389	20	AAW70853	Human Zcytor5 vari
44	2014	90.3	407	21	AAB19589	Mouse cytokine-lik
45	2014	90.3	407	22	AAB36648	Mouse cytokine rec

ALIGNMENTS

RESULT 1
AAY29779
ID AAY29779 standard; Protein; 410 AA.
XX
AC AAY29779;
XX
DT 04-NOV-1999 (first entry)
XX
DE Human DNAX soluble receptor subunit 1.
XX
KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
KW interleukin B30; DSRS1; DCRS1; IL-B30; cytokine receptor; diagnosis;
KW inflammatory disorder; inflammatory response; innate immunity;
KW morphogenic development; immunological disorder.
XX
OS Homo sapiens.
XX
PN WO9940195-A1.
XX
PD 12-AUG-1999.
XX
PF 05-FEB-1999; 99WO-US02600.
XX
PR 13-MAY-1998; 98US-0078194.
PR 06-FEB-1998; 98US-0073941.
XX
PA (SCHE) SCHERING CORP.
XX
PI Kastelein RA, Mattson JD, McClanahan TK;
XX
DR WPI; 1999-527306/44.
DR N-PSDB; AAZ08861.
XX

```
PT   New receptor subunits useful in the treatment inflammatory disorders
XX
PS   Claim 2; Page 22-23; 133pp; English.
XX
CC   The present invention describes a composition (I) comprising DNAX
CC   cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor
CC   subunit I (DSRS1) protein, which together encode a new mammalian
CC   cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)
CC   proteins, or DSRS1 and IL-B30 proteins. (I) comprising DSRS1 and DCRS1
CC   is useful for screening for ligands (i.e. agonists/antagonists) from
CC   a library of compounds, which are useful for modulating the physiology
CC   or development of a cell or tissue culture e.g. inflammatory responses,
CC   innate immunity and/or morphogenic development. (R), antibodies and
CC   ligands are useful for treatment of conditions, especially immunological
CC   disorders, associated with conditions exhibiting abnormal expression of
CC   (R). (R) is useful as a phosphate labeling enzyme to label substrates,
CC   and the subunits DSRS1 and DCRS1 are useful as immunogens for generating
CC   antibodies, or as antigens for binding antibodies. Nucleic acids
CC   encoding (R) are useful for identifying related DNAs and mRNAs, and
CC   variants from other individuals or species. The present sequence
CC   represents the specifically claimed human DSRS1, for use in the
CC   composition of the present invention.
XX
SQ   Sequence   410 AA;

  Query Match             100.0%;  Score 2230;  DB 20;  Length 410;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-181;
  Matches  410;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPDKL 410
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPDKL 410


RESULT 2
AAB19588
ID   AAB19588 standard; Protein; 410 AA.
XX
AC   AAB19588;
XX
DT   22-JAN-2001  (first entry)
XX
DE   Human cytokine-like factor-1.
XX
KW   Cytokine-like factor-1; CLF-1; interleukin-B60; IL-B60; human;
KW   cytokine; receptor; neuron; inflammation; antiinflammatory;
KW   autoimmune disease; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..38
FT                   /label= Signal_peptide
FT   Protein         39..410
FT                   /label= Mature_protein
FT   Domain          39..130
FT                   /note= "Ig-like domain"
FT   Domain          131..237
FT                   /note= "Ig-like domain"
FT   Domain          238..410
FT                   /note= "Ig-like domain"
XX
PN   WO200053631-A1.
XX
PD   14-SEP-2000.
XX
PF   09-MAR-2000; 2000WO-US06182.
XX
PR   11-MAR-1999;   99US-0267901.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Oppmann B, Timans JC, Kastelein RA, Bazan JF;
XX
DR   WPI; 2000-587426/55.
XX
PT   Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
PT   polypeptides, and nucleic acids, useful in research, diagnosis and for
PT   treating inflammatory and autoimmune disorders -
XX
PS   Claim 1; Page 21-22; 97pp; English.
XX
CC   The present sequence is that of human cytokine-like factor-1
CC   (CLF-1), a cytokine receptor family protein, which forms a complex
CC   with human interleukin-B60 (IL-B60, see AAB19586). The IL-B60/CLF-1
CC   cytokine serves as a key physiological factor in motor neuron
CC   development and regeneration. A claimed soluble complex comprises
CC   at least 6 amino acids of mature IL-60B, at least 6 amino acids of
CC   mature CLF-1 or at least 6 amino acids of mature CNTF-R. A claimed
CC   method of modulating the physiology or development of a cell or
CC   tissue culture cell involves contacting the cell with an agonist or
CC   antagonist of a complex comprising IL-60B and CLF-1 or CNTF-R. A
CC   claimed method of screening for a receptor which binds the complex
CC   involves contacting the complex with a cell expressing the receptor,
CC   to form a detectable interation resulting in a physiological
CC   response in the cell.
XX
SQ   Sequence   410 AA;

  Query Match             100.0%;  Score 2230;  DB 21;  Length 410;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-181;
  Matches  410;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
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Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPDKL 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPDKL 410


RESULT 3
AAB36647
ID   AAB36647 standard; Protein; 410 AA.
XX
AC   AAB36647;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Human cytokine receptor subunit NR6 protein SEQ ID NO:4.
XX
KW   Human; DNAX cytokine receptor subunit; DCRS2; receptor protein;
KW   modulating cell proliferation; diagnosis; detection; drug screening;
KW   immunological disorder.
XX
OS   Homo sapiens.
XX
PN   WO200073451-A1.
XX
PD   07-DEC-2000.
XX
PF   30-MAY-2000; 2000WO-US14867.
XX
PR   01-JUN-1999;   99US-0322913.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Dowling LM,  Timans JC,  Gorman DM,  Kastelein RA,  Bazan FJ;
XX
DR   WPI; 2001-061536/07.
XX
PT   Novel composition comprising DNAX cytokine receptor subunit polypeptide
PT   useful for regulating immune system function and for treating
PT   immunological disorders  -
XX
PS   Disclosure; Page 13-15; 93pp; English.
XX
CC   The present invention describes a composition (I) comprising a
CC   recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide.
CC   The DCRS2 polypeptide is useful for binding ligands and for preparing
CC   antibodies. The DCRS2 polypeptide is also useful for modulating cell
CC   proliferation, for diagnostic and therapeutic applications, for
CC   detecting presence of their ligands and in drug screening assays. It
CC   is also useful for treating conditions such as immunological disorders.
CC   The present sequence represents a cytokine receptor subunit protein
CC   which is given in an alignment of various cytokine receptor subunits in
CC   the exemplification of the present invention.
XX
SQ   Sequence   410 AA;

  Query Match           100.0%;  Score 2230;  DB 22;  Length 410;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-181;
  Matches  410;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPDKL 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPDKL 410


RESULT 4
AAY28281
ID   AAY28281 standard; Protein; 426 AA.
XX
AC   AAY28281;
XX
DT   30-SEP-1999  (first entry)
XX
DE   Amino acid sequence of a human H14 polypeptide.
XX
KW   Human; H14 polypeptide; cytokine receptor; ligand binding; control;
KW   cell surface localization; proliferation; differentiation; inhibitor;
KW   hematopoietic cell; hepatic cell; neural cell; osteoclastic cell;
KW   peptide fragmentation; isoelectric point; molecular weight marker;
KW   H14 counter-structure molecule.
XX
OS   Homo sapiens.
XX
PN   WO9935264-A1.
XX
PD   15-JUL-1999.
XX
PF   08-JAN-1999;   99WO-US00516.
XX
PR   09-JAN-1998;   98US-0070885.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cosman DJ,  Mosley B;
XX
DR   WPI; 1999-468840/39.
DR   N-PSDB; AAX89654.
XX
PT   H14 DNA, polypeptides and its fragments, useful as molecular weight
PT   markers
XX
PS   Claim 13; Page 7; 53pp; English.
XX
CC   The present sequence represents a human H14 polypeptide. H14 is a member
CC   of a family of cytokine receptors, which, after ligand binding and cell
CC   surface localization, induce proliferation, and/or differentiation of a
CC   wide variety of cell types including those of hematopoietic, hepatic,
CC   neural and osteoclastic origin. The H14 protein is used for the
CC   determination of the molecular weight of a sample protein. The protein
CC   and its fragments are useful as controls for peptide fragmentation. This
CC   is useful for determining the isoelectric point of a sample protein.
CC   Antibodies generated against H14 and its fragmented peptides can be used
CC   to enhance the accuracy of these molecular weight markers to determine
CC   the apparent molecular weight and isoelectric point of a sample protein.
CC   H14 can be used to screen for potential inhibitors of activity associated
CC   with H14 counter-structure molecules. H14 can also be used as therapeutic
CC   agents for the treatment of diseases mediated by H14.
XX
SQ   Sequence   426 AA;
```

```
  Query Match             99.2%;  Score 2212;  DB 20;  Length 426;
  Best Local Similarity   96.2%;  Pred. No. 1.2e-179;
  Matches  410;  Conservative    0;  Mismatches    0;  Indels   16;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---------------- 404
           ||||||||||||||||||||||||||||||||||||||||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQHRTRGSCPRADGARRE 420

Qy     405 VLPDKL 410
           ||||||
Db     421 VLPDKL 426
```

RESULT 5
AAY26339
ID AAY26339 standard; Protein; 422 AA.
XX
AC AAY26339;
XX
DT 13-JAN-2000 (first entry)
XX
DE Human U4 haematopoietin receptor superfamily chain-2.
XX
KW Human U4 protein; haematopoietin receptor superfamily;
KW biological activity; cytokine; cell proliferation; cell differentiation;
KW immune stimulation; immune suppression; haematopoiesis regulation;
KW immune disorder; immune deficiency; autoimmune disorder; allergy; cancer;
KW myeloid cell; lymphoid cell deficiency; platelet disorder.
XX
OS Homo sapiens.
XX
PN WO9953066-A1.
XX
PD 21-OCT-1999.
XX
PF 09-APR-1999; 99WO-US07882.
XX
PR 10-APR-1998; 98US-0058660.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Collins M, Donaldson D, Neben T, Whitters M;
XX
DR WPI; 1999-611303/52.
DR N-PSDB; AAX90754.
XX
PT Novel polypeptides and polynucleotides used for treatment of human
PT diseases and disorders e.g. immune disorders or deficiencies caused by
PT fungal, parasitic or viral infections -
XX
PS Claim 9; Pages 36-38; 43pp; English.
XX
CC The present sequence is a human U4 protein which is a member of
CC haematopoietin receptor superfamily.
CC The protein is predicted to have the following biological
CC activities: cytokine, cell proliferation/differentiation, immune
CC stimulating or suppressing and haematopoiesis regulating. The U4
CC protein can be used to treat immune disorders and deficiencies,
CC autoimmune disorders, allergies, cancer, myeloid or lymphoid cell
CC deficiencies and platelet disorders.
XX
SQ Sequence 422 AA;

```
  Query Match             98.8%;  Score 2202.5;  DB 20;  Length 422;
  Best Local Similarity   99.0%;  Pred. No. 7.6e-179;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           ||||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410
```

RESULT 6
AAY06479
ID AAY06479 standard; Protein; 422 AA.
XX
AC AAY06479;
XX
DT 27-SEP-1999 (first entry)
XX
DE Human tumour-associated protein PRO327.
XX
KW PRO327; UNQ288; cancer; tumour; diagnosis; therapy; human.
XX
OS Homo sapiens.
XX
PN WO9935170-A2.
XX
PD 15-JUL-1999.
XX
PF 05-JAN-1999; 99WO-US00106.
XX
PR 20-NOV-1998; 98US-0109304.
PR 05-JAN-1998; 98US-0070440.
PR 29-APR-1998; 98US-0083500.
PR 22-MAY-1998; 98US-0086414.
PR 10-JUN-1998; 98US-0088742.

```
PR   10-NOV-1998;   98US-0107783.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Goddard A,  Gurney AL,  Hillan KJ,  Lawrence DA;
PI   Roy MA,  Wood WI;
XX
DR   WPI; 1999-430385/36.
DR   N-PSDB; AAX87256.
XX
PT   Antibody against proteins expressed in neoplastic cells, useful for
PT   tumor diagnosis and treatment
XX
PS   Example 1; Fig 6; 162pp; English.
XX
CC   This sequence represents human PRO327 (UNQ288), a 46.3 kDa protein
CC   (pI 9.42) encoded by the novel cDNA clone DNA38113 (see AAX87256).
CC   Amplification of DNA38113 occurs in various lung and colon tumours
CC   and cell lines, suggesting a significant role in tumour formation
CC   and growth.  Antagonists (e.g. antibodies) directed against PRO327
CC   are expected to have utility in cancer therapy.  The invention
CC   identifies 14 genes (see AAX87254-67) that are amplified in the
CC   genome of tumour cells.  Such amplification is expected to be
CC   associated with overexpression of the gene product and to contribute
CC   to tumorigenesis.  The encoded proteins (see AAY06477-90) may be
CC   useful targets for the diagnosis and/or treatment (including
CC   prevention) of certain cancers, and may act as predictors of the
CC   prognosis of tumour treatment.  Antibodies that bind the proteins
CC   are claimed and used in claimed cancer diagnostic kits.
XX
SQ   Sequence   422 AA;

  Query Match             98.8%;  Score 2202.5;  DB 20;  Length 422;
  Best Local Similarity   99.0%;  Pred. No. 7.6e-179;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           |||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 7
AAY17825
ID   AAY17825 standard; Protein; 422 AA.
XX
AC   AAY17825;
XX
DT   12-AUG-1999  (first entry)
XX
DE   Human PRO327 protein sequence.
XX
KW   Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
KW   secreted protein; transmembrane protein; inflammation disorder.
XX
OS   Homo sapiens.
XX
PN   WO9928462-A2.
XX
PD   10-JUN-1999.
XX
PF   01-DEC-1998;   98WO-US25108.
XX
PR   25-FEB-1998;   98US-0075945.
PR   03-DEC-1997;   97US-0067411.
PR   11-DEC-1997;   97US-0069278.
PR   11-DEC-1997;   97US-0069334.
PR   11-DEC-1997;   97US-0069335.
PR   12-DEC-1997;   97US-0069425.
PR   16-DEC-1997;   97US-0069694.
PR   16-DEC-1997;   97US-0069696.
PR   16-DEC-1997;   97US-0069702.
PR   17-DEC-1997;   97US-0069870.
PR   17-DEC-1997;   97US-0069873.
PR   18-DEC-1997;   97US-0068017.
PR   05-JAN-1998;   98US-0070440.
PR   09-FEB-1998;   98US-0074086.
PR   09-FEB-1998;   98US-0074092.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Chen J,  Goddard A,  Gurney AL,  Wood WI;
PI   Yuan J;
XX
DR   WPI; 1999-371118/31.
DR   N-PSDB; AAX80050.
XX
PT   Nucleic acids encoding PRO secreted and transmembrane proteins
XX
PS   Claim 12; Fig 17; 123pp; English.
XX
CC   The present invention describes nucleic acids encoding PRO secreted and
CC   transmembrane proteins used therapeutically. The PRO proteins have
CC   cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
CC   activity. The proteins and polynucleotides can be used in therapy,
CC   identification of homologues, raising antibodies and design of probes
CC   and primers. They can be used in a range of diseases related to proteins
CC   that they have homology with, e.g. a PRO protein having homology to
CC   complement proteins may be used in inflammatory responses.
XX
SQ   Sequence   422 AA;

  Query Match             98.8%;  Score 2202.5;  DB 20;  Length 422;
  Best Local Similarity   99.0%;  Pred. No. 7.6e-179;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
```

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
          |||||||||||||||||||||||||||||||||||||||||||   :||
Db    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 8
AAY05782
ID   AAY05782 standard; Protein; 422 AA.
XX
AC   AAY05782;
XX
DT   02-AUG-1999  (first entry)
XX
DE   Human type 1 cytokine receptor GBRI-ILR.
XX
KW   GBRI-ILR; hGBR-ILR; cytokine receptor; human; cancer; obesity;
KW   inflammation; septic shock; AIDS; embryo development;
KW   lung infection; cytostatic; anorectic; immunosuppressive;
KW   antibacterial; antiviral; antiinflammatory; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..37
FT                   /note= "signal peptide"
FT   Protein         38..422
FT                   /note= "mature protein; a polypeptide comprising
FT                          amino acids 38-422 is also claimed in Claim
FT                          1a"
XX
PN   WO9920755-A2.
XX
PD   29-APR-1999.
XX
PF   14-OCT-1998;   98WO-EP06497.
XX
PR   16-OCT-1997;   97GB-0021961.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Elson G,  Gauchat J,  Kosco-Vilbois M;
XX
DR   WPI; 1999-288305/24.
DR   N-PSDB; AAX25489.
XX
PT   Novel human or mouse type I cytokine receptors hGBRI-ILR or
PT   mGBRI-ILR, useful for treating e.g. cancer, immune disorders,
PT   obesity and AIDS
XX
PS   Claim 1a; Fig 4; 41pp; English.
XX
CC   The present sequence represents a novel type 1 cytokine receptor
CC   that has been termed human GBRI-ILR as it is believed to be an
CC   interleukin receptor, or at least a substantial part of such a
CC   receptor.  The sequence is predicted from an isolated full-length
CC   cDNA clone (see AAX25489) obtained from a human placental cDNA
CC   library.  GBRI-ILR mRNA is expressed most strongly in spleen,
CC   thymus, lymph node, appendix, bone marrow, thyroid, adrenal
CC   cortex, stomach, heart, placenta and skeletal muscle, suggesting a
CC   role for GBRI-ILR in the immune system.  In human foetal tissue,
CC   strong expression is seen in the lung, but not in brain, kidney or
CC   liver.  A GBRI-ILR receptor has also been identified in mice (see
CC   AAY05783).  The high degree of conservation of amino acids between
CC   the human and murine polypeptides indicates that this receptor is
CC   functionally important.  GBRI-ILR polypeptides, nucleic acids,
CC   antibodies, agonists and antagonists can be used to treat e.g.
CC   cancer, immune disorders, obesity (in view of homology to the
CC   leptin receptor), embryonic developmental disorders, AIDS, septic
CC   shock and lung infection (claimed).
XX
SQ   Sequence   422 AA;

  Query Match             98.8%;  Score 2202.5;  DB 20;  Length 422;
  Best Local Similarity   99.0%;  Pred. No. 7.6e-179;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy      1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy     61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy    121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy    181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy    241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
          |||||||||||||||||||||||||||||||||||||||||||   :||
Db    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 9
AAY93686
ID   AAY93686 standard; Protein; 422 AA.
XX
AC   AAY93686;
XX
DT   03-OCT-2000  (first entry)
XX
DE   Amino acid sequence of novel polypeptide PRO327.
XX
KW   PRO201; PRO292; PRO327; PRO1265;  PRO344; PRO343; PRO347; PRO357;
KW   PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
KW   tumourigenesis; cancer; neoplastic cell growth; cell proliferation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT                   /note= "signal sequence"
FT   Modified-site   3..7
FT                   /note= "amidation site"
FT   Modified-site   30..36
FT                   /note= "N-myristoylation site"
FT   Modified-site   37..43
FT                   /note= "N-myristoylation site"
FT   Modified-site   44..48
FT                   /note= "casein kinase II phosphorylation site"
FT   Modified-site   73..79
FT                   /note= "N-myristoylation site"
FT   Modified-site   79..83
FT                   /note= "amidation site"
FT   Modified-site   92..96
FT                   /note= "N-glycosylation site"
FT   Modified-site   104..108
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FT                   /note= "N-glycosylation site"
FT   Modified-site   121..127
FT                   /note= "N-myristoylation site"
FT   Modified-site   140..144
FT                   /note= "N-glycosylation site"
FT   Modified-site   168..172
FT                   /note= "N-glycosylation site"
FT   Modified-site   179..185
FT                   /note= "N-myristoylation site"
FT   Modified-site   183..187
FT                   /note= "casein kinase II phosphorylation site"
FT   Modified-site   205..209
FT                   /note= "casein kinase II phosphorylation site"
FT   Modified-site   218..224
FT                   /note= "N-myristoylation site"
FT   Modified-site   292..296
FT                   /note= "N-glycosylation site"
FT   Modified-site   300..306
FT                   /note= "N-myristoylation site"
F[redacted]Modified-site   317..323
F                    /note= "N-myristoylation site"
FT   Modified-site   320..326
FT                   /note= "N-myristoylation site"
FT   Modified-site   325..332
FT                   /note= "Growth factor and cytokines receptor
FT                    family signature 2"
FT   Modified-site   347..353
FT                   /note= "N-myristoylation site"
FT   Modified-site   355..361
FT                   /note= "N-myristoylation site"
FT   Modified-site   382..386
FT                   /note= "N-glycosylation site"
FT   Modified-site   407..413
FT                   /note= "N-myristoylation site"
FT   Modified-site   411..415
FT                   /note= "amidation site"
FT   Modified-site   413..417
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                    phosphorylation site"
XX
PN   WO200037640-A2.
XX
PD   29-JUN-2000.
XX
PF   16-DEC-1999;   99WO-US30095.
XX
PR   22-DEC-1998;   98US-0113296.
P[redacted]08-MAR-1999;   99WO-US05028.
P[redacted]02-JUN-1999;   99WO-US12252.
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   30-NOV-1999;   99WO-US28313.
PR   30-NOV-1999;   99WO-US28409.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Goddard A,  Gurney AL,  Hillan K,  Lawrence DA,  Roy MA;
PI   Wood WI;
XX
DR   WPI; 2000-452188/39.
DR   N-PSDB; AAA46902.
XX
PT   New anti-polypeptide antibody useful in the treatment and diagnosis of
PT   neoplastic cell growth and proliferation -
XX
PS   Claim 61; Fig 6; 220pp; English.
XX
CC   The present sequence represents a novel human polypeptide. The
CC   specification describes novel polypeptides designated PRO201, PRO292,
CC   PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO715, PRO1017,
CC   PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in
CC   the genome of tumour cells. The polypeptides are believed to contribute
CC   to tumourigenesis. The polypeptides are useful target for the
CC   identification of certain cancers, and may act as predictors of the
CC   prognosis of tumour treatment. Antibodies against these polypeptides
CC   are useful in the treatment and diagnosis of neoplastic cell growth
CC   and proliferation in mammals.
XX
SQ   Sequence   422 AA;

  Query Match             98.8%;  Score 2202.5;  DB 21;  Length 422;
  Best Local Similarity   99.0%;  Pred. No. 7.6e-179;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           |||||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 10
AAB01316
ID   AAB01316 standard; Protein; 422 AA.
XX
AC   AAB01316;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Human PRO327 polypeptide.
XX
KW   PRO; membrane bound protein; secreted protein; PRO357; PRO327;
KW   PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347;
KW   PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
KW   antibody; screening; detection; inhibition; probe; primer; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT                   /label= Signal peptide
FT   Modified-site   3..7
FT                   /note= "Amidation site"
FT   Modified-site   30..36
FT                   /note= "N-myristoylation site"
FT   Modified-site   37..43
FT                   /note= "N-myristoylation site"
FT   Domain          44..61
FT                   /label= Transmembrane domain
FT   Modified-site   73..79
FT                   /note= "N-myristoylation site"
FT   Modified-site   79..83
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FT                   /note= "Amidation site"
FT   Modified-site   92..96
FT                   /note= "N-glycosylation site"
FT   Modified-site   104..108
FT                   /note= "N-glycosylation site"
FT   Modified-site   121..127
FT                   /note= "N-myristoylation site"
FT   Modified-site   140..144
FT                   /note= "N-glycosylation site"
FT   Modified-site   168..172
FT                   /note= "N-glycosylation site"
FT   Modified-site   179..185
FT                   /note= "N-myristoylation site"
FT   Modified-site   218..224
FT                   /note= "N-myristoylation site"
FT   Modified-site   292..296
FT                   /note= "N-glycosylation site"
FT   Modified-site   300..306
FT                   /note= "N-myristoylation site"
FT   Modified-site   317..323
FT                   /note= "N-myristoylation site"
F[redacted] Modified-site   320..326
F                    /note= "N-myristoylation site"
FT   Region          325..331
FT                   /label= Growth factor/cytokine receptor family
FT                          signature
FT   Modified-site   347..353
FT                   /note= "N-myristoylation site"
FT   Modified-site   355..361
FT                   /note= "N-myristoylation site"
FT   Modified-site   382..386
FT                   /note= "N-glycosylation site"
FT   Modified-site   407..413
FT                   /note= "N-myristoylation site"
FT   Modified-site   413..417
FT                   /note= "cAMP and cGMP-dependent protein kinase
FT                          phosphorylation site"
XX
PN   WO200032776-A2.
XX
PD   08-JUN-2000.
XX
PF   01-DEC-1999;   99WO-US28301.
XX
PR   01-DEC-1998;   98WO-US25108.
PR   16-DEC-1998;   98US-0112850.
PR   22-DEC-1998;   98US-0113296.
XX
P[redacted] (GETH ) GENENTECH INC.
XX
P[redacted] Baker KP,  Botstein D,  Eaton DL,  Ferrara N,  Filvaroff E;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Grimaldi CJ,  Gurney AL;
PI   Hillan KJ,  Kljavin IJ,  Napier MA,  Roy MA,  Tumas D,  Wood WI;
XX
DR   WPI; 2000-412324/35.
DR   N-PSDB; AAA49558.
XX
PT   New human nucleic acids encoding secreted and transmembrane
PT   polypeptides, designated as PRO polypeptides, useful as pharmaceutical
PT   and diagnostic agents
XX
PS   Claim 12; Fig 14; 187pp; English.
XX
CC   New human nucleic acids encoding secreted and transmembrane
CC   polypeptides which are designated as PRO polypeptides are described
CC   The membrane-bound proteins have various industrial applications,
CC   including as pharmaceutical and diagnostic agents. The membrane-bound
CC   proteins can also be employed for screening of potential peptide or
CC   small molecule inhibitors of the relevant receptor/ligand interaction.
CC   Anti-PRO antibodies are useful for the affinity purification of PRO
CC   from recombinant cell culture or natural sources.
XX
SQ   Sequence   422 AA;
```

```
  Query Match             98.8%;  Score 2202.5;  DB 21;  Length 422;
  Best Local Similarity   99.0%;  Pred. No. 7.6e-179;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           ||||||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410
```

```
RESULT 11
AAG63545
ID   AAG63545 standard; Protein; 422 AA.
XX
AC   AAG63545;
XX
DT   15-OCT-2001  (first entry)
XX
DE   Amino acid sequence of a human CLF-1 protein.
XX
KW   NNT-1; CLF-1; sCNTFRalpha; nervous system; neuron; nervous system;
KW   neuro-muscular function; tumour; immune system; haematopoietic system;
KW   reproductive system; liver; skeletal muscle; neurodegenerative disease;
KW   amyotrophic lateral sclerosis; Parkinson's disease; Huntingdon's disease;
KW   muscular mass; paralysis; cancer; obesity; fertility; endometriosis;
KW   blastocyst implantation; thrombosis; retinal disease;
KW   retinal pigmentosis.
XX
OS   Homo sapiens.
XX
PN   WO200155172-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001; 2001WO-FR00253.
XX
PR   27-JAN-2000; 2000FR-0001035.
PR   12-OCT-2000; 2000FR-0013089.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI   Elson G,  Gauchat J,  Plun-Favreau H,  Chevalier S,  Gascan H;
XX
DR   WPI; 2001-488773/53.
DR   N-PSDB; AAH74486.
XX
PT   A complex comprising a NNT-1 protein and a CLF-1 and/or sCNTFRalpha
PT   protein useful to treat neurodegenerative disease including Parkinson's
```

```
PT   and Huntington's, obesity and cancer  -
XX
PS   Claim 2; Page 63-64; 67pp; French.
XX
CC   The present sequence represents a human CLF-1 protein. The specification
CC   describes a complex comprising a NNT-1 protein and a CLF-1 and/or
CC   sCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate
CC   activity of the sCNTFRalpha/gp130/LIFRbeta receptor complex, or to
CC   induce phosphorylation of the tyrosine of gp130 and LIFRbeta,
CC   particularly where cells expressing the receptor complex are in the
CC   central or peripheral nervous system, in neurons implicated in
CC   neuro-muscular function or in skeletal muscle. The complex or
CC   antibodies are also used to decrease the survival, growth or
CC   proliferation of tumour cells or to facilitate the proliferation and/or
CC   inhibit differentiation of cells stocks. The complex is also used to
CC   modulate activity of the gp130/LIFRbeta receptor or cells expressing
CC   that receptor, particularly those cells implicated in the immune,
CC   haematopoietic, nervous or reproductive system, the liver or skeletal
CC   muscle. Molecules of the invention may be used to prevent or treat
C    neurodegenerative diseases including amyotrophic lateral sclerosis,
C    Parkinson's and Huntington's disease, to repair or regenerate nervous
CC   or muscular tissue or to maintain muscular mass in paralysis patients.
CC   They may also be used to treat cancer, obesity and associated diseases,
CC   and to improve fertility, particularly to avoid endometriosis and/or
CC   assist blastocyst implantation, thrombosis, or retinal disease,
CC   particular retinal pigmentosis.
XX
SQ   Sequence   422 AA;

  Query Match             98.8%;  Score 2202.5;  DB 22;  Length 422;
  Best Local Similarity   99.0%;  Pred. No. 7.6e-179;
  Matches  406;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps    1;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
D      181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           |||||||||||||||||||||||||||||||||||||||||||   :||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410


RESULT 12
AAG63544
ID   AAG63544 standard; Protein; 445 AA.
XX
AC   AAG63544;
XX
DT   15-OCT-2001  (first entry)
XX
DE   Amino acid sequence of a human CLF-1 protein.
XX
KW   NNT-1; CLF-1; sCNTFRalpha; nervous system; neuron; nervous system;
KW   neuro-muscular function; tumour; immune system; haematopoietic system;
KW   reproductive system; liver; skeletal muscle; neurodegenerative disease;
KW   amyotrophic lateral sclerosis; Parkinson's disease; Huntingdon's disease;
KW   muscular mass; paralysis; cancer; obesity; fertility; endometriosis;
KW   blastocyst implantation; thrombosis; retinal disease;
KW   retinal pigmentosis.
XX
OS   Homo sapiens.
XX
PN   WO200155172-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001; 2001WO-FR00253.
XX
PR   27-JAN-2000; 2000FR-0001035.
PR   12-OCT-2000; 2000FR-0013089.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI   Elson G,  Gauchat J,  Plun-Favreau H,  Chevalier S,  Gascan H;
XX
DR   WPI; 2001-488773/53.
DR   N-PSDB; AAH74485.
XX
PT   A complex comprising a NNT-1 protein and a CLF-1 and/or sCNTFRalpha
PT   protein useful to treat neurodegenerative disease including Parkinson's
PT   and Huntington's, obesity and cancer  -
XX
PS   Claim 2; Page 60-61; 67pp; French.
XX
CC   The present sequence represents a human CLF-1 protein. The specification
CC   describes a complex comprising a NNT-1 protein and a CLF-1 and/or
CC   sCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate
CC   activity of the sCNTFRalpha/gp130/LIFRbeta receptor complex, or to
CC   induce phosphorylation of the tyrosine of gp130 and LIFRbeta,
CC   particularly where cells expressing the receptor complex are in the
CC   central or peripheral nervous system, in neurons implicated in
CC   neuro-muscular function or in skeletal muscle. The complex or
CC   antibodies are also used to decrease the survival, growth or
CC   proliferation of tumour cells or to facilitate the proliferation and/or
CC   inhibit differentiation of cells stocks. The complex is also used to
CC   modulate activity of the gp130/LIFRbeta receptor or cells expressing
CC   that receptor, particularly those cells implicated in the immune,
CC   haematopoietic, nervous or reproductive system, the liver or skeletal
CC   muscle. Molecules of the invention may be used to prevent or treat
CC   neurodegenerative diseases including amyotrophic lateral sclerosis,
CC   Parkinson's and Huntington's disease, to repair or regenerate nervous
CC   or muscular tissue or to maintain muscular mass in paralysis patients.
CC   They may also be used to treat cancer, obesity and associated diseases,
CC   and to improve fertility, particularly to avoid endometriosis and/or
CC   assist blastocyst implantation, thrombosis, or retinal disease,
CC   particular retinal pigmentosis.
XX
SQ   Sequence   445 AA;

  Query Match             98.7%;  Score 2200;  DB 22;  Length 445;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-178;
  Matches  404;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
```

```
Qy    181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy    241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ 404
          |||||||||||||||||||||||||||||||||||||||||||||
Db    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ 404
```

RESULT 13
ABB06125
ID ABB06125 standard; Protein; 457 AA.
XX
AC ABB06125;
XX
DT 10-MAY-2002 (first entry)
XX
DE Human NS protein sequence SEQ ID NO:217.
XX
KW Human; cytostatic; osteopathic; gynaecological; neuroprotective;
KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KW anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;
KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
KW anticonvulsant; antidiabetic; tranquilliser; antidepressant; aeuroleptic;
KW gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;
KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KW infertility; cardiovascular disease; coagulation disease; hypertension;
KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KW gastric ulcer; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200206315-A2.
XX
PD 24-JAN-2002.
XX
[redacted] 17-JUL-2001; 2001WO-IL00653.
XX
PR 18-JUL-2000; 2000IL-0137345.
PR 15-DEC-2000; 2000IL-0140354.
XX
PA (COMP-) COMPUGEN LTD.
XX
PI Mintz L, Freilich S, Bernstein J;
XX
DR WPI; 2002-155037/20.
DR N-PSDB; ABL39779.
XX
PT One hundred and twenty eight novel nucleic acid sequences, useful for
PT treating and diagnosing e.g. cancer, asthma and Alzheimer's -
XX
PS Claim 6; Page 253-254; 290pp; English.
XX
CC ABL39691 to ABL39818 represent novel human nucleic acid sequences
CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
CC anorectic, muscular, anti-HIV, antiinfertility, cardiovascular,
CC anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant,
CC immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antiulcer,
CC antidepressant, gastrointestinal, aeuroleptic, cerebroprotective,
CC nootropic and contraceptive activities. The NS can be used in vaccines,
CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
CC antibodies from the present invention can be used for treating and
CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC Alzheimer's disease and as a contraceptive.
XX
SQ Sequence 457 AA;

```
  Query Match             98.7%;  Score 2200;  DB 23;  Length 457;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-178;
  Matches  404;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy     61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy    121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy    181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240

Qy    241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ 404
          |||||||||||||||||||||||||||||||||||||||||||||
Db    361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ 404
```

RESULT 14
AAW70860
ID AAW70860 standard; Protein; 422 AA.
XX
AC AAW70860;
XX
DT 17-MAR-1999 (first entry)
XX
DE Human Zcytor5 protein sequence.
XX
KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; Zcytor5 ligand.
XX
OS Homo sapiens.
XX
PN WO9849307-A1.
XX
PD 05-NOV-1998.
XX
PF 01-MAY-1998; 98WO-US08865.
XX
PR 13-FEB-1998; 98US-0074721.
PR 01-MAY-1997; 97US-0045287.

PR 01-MAY-1997; 97US-0850030.
PR 13-FEB-1998; 98US-0023890.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM;
PI Lok S, Presnell SR, Whitmore TE;
XX
DR WPI; 1999-034662/03.
DR N-PSDB; AAV70894.
XX
PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
PT down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
PT in blood
XX
PS Claim 1; Page 66-67; 55pp; English.
XX
CC The present sequence represents a protein designated Zcytor5, which is
CC a cytokinin-like receptor. Soluble Zcytor5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcytor5 ligands. A probe
CC comprising Zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcytor5 and
CC therapeutically to modify Zcytor5 ligand effects.
XX
SQ Sequence 422 AA;

Query Match 98.6%; Score 2198.5; DB 20; Length 422;
Best Local Similarity 98.8%; Pred. No. 1.7e-178;
Matches 405; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

```
Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPE 240

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360

Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLP 407
           ||||||||||||||||||||||||||||||||||||||||   :||
Db     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILP 410
```

RESULT 15
AAW70861
ID AAW70861 standard; Protein; 425 AA.
XX
AC AAW70861;
XX
DT 17-MAR-1999 (first entry)
XX
DE Allelic varaint of human Zcytor5.
XX
KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-1;
KW cardiac pathology; heart enlargement; Zcytor5 ligand; allelic varaint.
XX
OS Homo sapiens.
XX
PN WO9849307-A1.
XX
PD 05-NOV-1998.
XX
PF 01-MAY-1998; 98WO-US08865.
XX
PR 13-FEB-1998; 98US-0074721.
PR 01-MAY-1997; 97US-0045287.
PR 01-MAY-1997; 97US-0850030.
PR 13-FEB-1998; 98US-0023890.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner JM;
PI Lok S, Presnell SR, Whitmore TE;
XX
DR WPI; 1999-034662/03.
DR N-PSDB; AAV70895.
XX
PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
PT down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
PT in blood
XX
PS Claim 1; Page 71-72; 55pp; English.
XX
CC The present sequence represents an allelic varaint of protein designated
CC Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be
CC administered to down-regulate the effects of a growth and/or maintenance
CC factor in thyroid, heart, and skeletal muscle for example to lessen the
CC effect of cardiotrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
CC blood, and to discover other possible Zcytor5 ligands. A probe
CC comprising Zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcytor5 and
CC therapeutically to modify Zcytor5 ligand effects.
XX
SQ Sequence 425 AA;

Query Match 98.5%; Score 2197.5; DB 20; Length 425;
Best Local Similarity 96.0%; Pred. No. 2e-178;
Matches 409; Conservative 0; Mismatches 0; Indels 17; Gaps 2;

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Qy       1 MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1 MPAGRRGPAAQSARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 59

Qy      61 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD 119

Qy     121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     120 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ 179

Qy     181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 239

Qy     241 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG 299

Qy     301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 359
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Qy     361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---------------- 404
           ||||||||||||||||||||||||||||||||||||||||||||||
Db     360 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQHRTRGSCPRADGARRE 419

Qy     405 VLPDKL 410
           ||||||
Db     420 VLPDKL 425
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Search completed: March 13, 2003, 11:49:19
Job time : 45.296 secs